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(54) **ANTI-SERUM ALBUMIN BINDING VARIANTS**

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(75) Inventors: **Elena De Angelis**, Cambridge (GB); **Carolyn Enever**, Cambridge (GB); **Haiqun Liu**, Cambridge (GB); **Oliver Schon**, Cambridge (GB)

(58) **Field of Classification Search**  
None  
See application file for complete search history.

(73) Assignee: **GLAXO GROUP LIMITED** (GB)

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(\* ) Notice: Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 667 days.  
  
This patent is subject to a terminal disclaimer.

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*Primary Examiner* — Brad Duffy  
*Assistant Examiner* — Nelson B Moseley, II  
(74) *Attorney, Agent, or Firm* — Jason C. Fedon; William T. Han

(57) **ABSTRACT**

The invention relates to improved variants of the anti-serum albumin immunoglobulin single variable domain DOM7h-14, as well as ligands and drug conjugates comprising such variants, compositions, nucleic acids, vectors and hosts.

**28 Claims, 6 Drawing Sheets**

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human	kinetics based on DOM7h-14 and DOM7h-11 lineage (ranges supported by data)		
	<b>overall range</b>		
	KD: 1 to 10000		
	Kd: 1.5e-4 to 0.1 ; Ka: 2e6 to 1e4		
<b>therapeutic ranges</b>	chronic	intermediate	acute
	high affinity	medium affinity	low affinity
	KD: 0.1-400	KD: 400-2000	KD: 2000-10000
	Kd: 1.5e-4 to 8e-3 ; Ka: 1e6 to 5e4	Kd: 8e-3 to 0.08 ; Ka: 2e4 to 5e4	Kd: 0.08 to 0.1 ; Ka: 5e4 to 1e4
optional ranges	KD: 1-200	KD: 400-1500	KD: 2000-6000
	Kd: 3e-4 to 2e-3; Ka: 1e6 to 5e4	Kd: 8e-3 to 0.08; Ka: 2e4 to 6e4	Kd: 0.08 to 0.1 ; Ka: 5e4 to 2e4
Examples	DOM7h-11-15, DOM7h-14, DOM7h-14-10, DOM7h-14-18, DOM7h-14-19, DOM7h-11-18, DOM7h-11-19, DMS7321, DMS7322; DMS7324, DMS7327	DMS7325, DMS7326; DMS7323	DOM7h-11

Figure 2A

<b>Cyno</b>			
	<b>overall range</b>		
	KD: 1 to 10000		
	Kd:1.5e-4 to 0.1 ; Ka:2e6 to 1e4		
<b>therapeutic ranges</b>	chronic	intermediate	acute
	high affinity	medium affinity	low affinity
	KD: 0.1-400	KD: 400-2000	KD: 2000-10000
	Kd:1.5e-4 to 8e-3 ; Ka:2e6 to 2e4	Kd: 8e-3 to 0.08 ; Ka: 2e4 to 5e4	Kd:0.08 to 0.1 ; Ka: 5e4 to 1e4
<b>optional ranges</b>	KD: 1-200	KD: 400-1500	KD: 2000-6000
	Kd:3e-4 to 2e-3; Ka: 1e6 to 1e4	Kd:2e-3 to 0.05; Ka: 2e4 to 1e4	Kd:0.08 to 0.1 ; Ka: 5e4 to 2e4
<b>Examples</b>	DMS7327; DOM7h-11-15; DOM7h-14; DOM7h-14-10; DOM7h-14-18; DOM7h-14-19, DOM7h-14-28, DOM7h-14-36 DMS7321; DMS7322	DOM7h-11; DMS7326; DMS7324;	DOM7h11-12, DOM7h-11-18 DMS7325

Figure 2B

Rat			
	<b>overall range</b>		
	KD: 1 to 10000		
	Kd: 2e-3 to 0.15 ; Ka: 2e6 to 1e4		
<b>therapeutic ranges</b>	chronic	intermediate	acute
	high affinity	medium affinity	low affinity
	KD: 1-300	KD: 300-2000	KD: 2000-10000
	Kd:2e-3 to 5e-2 ; Ka:2e6 to 2e5	Kd:5e-2 to 0.09 ; Ka:2e5 to 4.5e4	Kd:0.09 to 0.15 ; Ka: 4.5e4 to 1.5e4
optional ranges	KD: 20-200	KD: 400-1800	KD: 2000-6000
	Kd:9e-3 to 2e-2 ; Ka: 1e6 to 1e5	Kd: 4e-2 to 0.09; Ka:1e5 to 5e4	Kd: 0.1 to 0.14 ; Ka: 5e4 to 3e4
Examples	DOM7h-11-15; DOM7h-11-12; DOM7h-11-18, DOM7h-11-19, DOM7h-14-28, DOM7h-14-36, DOM7h-14 DMS7327; DMS7322	DOM7h-14-18; DOM7h-14-19; DMS7321; DMS7323, DMS7324, DMS7326,;	DMS7325; DOM7h-11;

Figure 2C

<b>Mouse</b>			
	<b>overall range</b>		
	KD: 1 to 10000		
	Kd: 2e-3 to 0.15 ; Ka: 2e6 to 1e4		
<b>therapeutic ranges</b>	chronic	intermediate	acute
	high affinity	medium affinity	low affinity
	KD: 1-100	KD: 100-2000	KD: 2000-10000
	Kd:2e-3 to 1e-2 ; Ka:2e6 to 1e5	Kd:1e-2 to 0.07 ; Ka: 1e5 to 3e4	Kd: 0.08 to 0.15; Ka: 4e4 to 1.5e4
<b>optional ranges</b>	KD: 1 to 80	KD: 120-2000	KD: 4000-10000
	Kd:2e-3 to 1e-2 ; Ka: 2e6 to 1.5e5	Kd: 9e-3 to 0.07 ; Ka: 1.3e5 to 3e4	Kd:0.1 to 0.15 ; Ka: 2.5e4 to 1.5e4
<b>Examples</b>	DOM7h-11-15;; DOM7h-14; DOM7h-14-10, DOM7h-14-18, DOM7h-14-19, DOM7h-11-18, DOM7h-11-19, DOM7h-14-28, DOM7h-14-36 DMS7322, DMS7327	DMS7321; DMS7323; DMS7324; DOM7h-11-12; DMS7326	DMS7325; DOM7h-11

Figure 2D

## ANTI-SERUM ALBUMIN BINDING VARIANTS

This application is a 371 of International Application No. PCT/EP2010/052007, filed 17 Feb. 2010, which claims the benefit of U.S. Provisional Application Nos. 61/153,746, filed 19 Feb. 2009, and 61/163,990, filed 27 Mar. 2009, which are incorporated herein in their entirety.

The invention relates to improved variants of the anti-serum albumin immunoglobulin single variable domain DOM7h-14, as well as ligands and drug conjugates comprising such variants, compositions, nucleic acids, vectors and hosts.

### BACKGROUND OF THE INVENTION

WO04003019 and WO2008/096158 disclose anti-serum albumin (SA) binding moieties, such as anti-SA immunoglobulin single variable domains (dAbs), which have therapeutically-useful half-lives. These documents disclose monomer anti-SA dAbs as well as multi-specific ligands comprising such dAbs, eg, ligands comprising an anti-SA dAb and a dAb that specifically binds a target antigen, such as TNFR1. Binding moieties are disclosed that specifically bind serum albumins from more than one species, eg human/mouse cross-reactive anti-SA dAbs.

WO05118642 and WO2006/059106 disclose the concept of conjugating or associating an anti-SA binding moiety, such as an anti-SA immunoglobulin single variable domain, to a drug, in order to increase the half-life of the drug. Protein, peptide and NCE (new chemical entity) drugs are disclosed and exemplified. WO2006/059106 discloses the use of this concept to increase the half-life of insulintropic agents, eg, incretin hormones such as glucagon-like peptide (GLP)-1.

Reference is also made to Holt et al, "Anti-Serum albumin domain antibodies for extending the half-lives of short lived drugs", Protein Engineering, Design & Selection, vol 21, no 5, pp 283-288, 2008.

WO2008/096158 discloses DOM7h-14, which is a good anti-SA dAb. It would be desirable to provide improved dAbs that are variants of DOM7h-14 and that specifically bind serum albumin, preferably albumins from human and non-human species, which would provide utility in animal models of disease as well as for human therapy and/or diagnosis. It would also be desirable to provide for the choice between relatively modest- and high-affinity anti-SA binding moieties (dAbs). Such moieties could be linked to drugs, the anti-SA binding moiety being chosen according to the contemplated end-application. This would allow the drug to be better tailored to treating and/or preventing chronic or acute indications, depending upon the choice of anti-SA binding moiety. It would also be desirable to provide anti-dAbs, that are monomeric or substantially so in solution. This would especially be advantageous when the anti-SA dAb is linked to a binding moiety, eg, a dAb, that specifically binds a cell-surface receptor, such as TNFR1, with the aim of antagonizing the receptor. The monomeric state of the anti-SA dAb is useful in reducing the chance of receptor cross-linking, since multimers are less likely to form which could bind and cross-link receptors (eg, TNFR1) on the cell surface, thus increasing the likelihood of receptor agonism and detrimental receptor signaling.

### SUMMARY OF THE INVENTION

Aspects of the present invention solve these problems.

To this end, the present inventors surprisingly found that beneficial mutations can be targeted to the CDR3 region 92 to 96 (position numbering according to Kabat) compared to DOM7h-14.

In one aspect the invention, therefore, provides an anti-serum albumin (SA) immunoglobulin single variable domain variant of DOM7h-14, wherein the variant comprises at least one mutation in CDR3 region 92 to 96 (position numbering according to Kabat) compared to DOM7h-14, and wherein the variant has from 1 to 8 changes compared to the amino acid sequence of DOM7h-14. There is also provided an anti-serum albumin (SA) binding moiety comprising CDR3 of a variant of this aspect of the invention.

Another aspect of the invention provides an anti-serum albumin (SA) immunoglobulin single variable domain variant of DOM7h-14, wherein the variant comprises a Ser at position 22 and a Glu at position 42 (numbering according to Kabat) compared to DOM7h-14, and wherein the variant has from 0 to 4 further changes compared to the amino acid sequence of DOM7h-14.

Embodiments of any aspect of the invention provide DOM7h-14 variants of good anti-serum albumin affinities. The choice of variant can allow for tailoring of half-life according to the desired therapeutic and/or prophylactic setting. For example, in one embodiment, the affinity of the variant for serum albumin is relatively high, such that the variant would be useful for inclusion in products that find utility in treating and/or preventing chronic or persistent diseases, conditions, toxicity or other chronic indications. In one embodiment, the affinity of the variant for serum albumin is relatively modest, such that the variant would be useful for inclusion in products that find utility in treating and/or preventing acute diseases, conditions, toxicity or other acute indications. In one embodiment, the affinity of the variant for serum albumin is intermediate, such that the variant would be useful for inclusion in products that find utility in treating and/or preventing acute or chronic diseases, conditions, toxicity or other acute or chronic indications.

It is conceivable that a molecule with an appropriately high affinity and specificity for serum albumin would stay in circulation long enough to have the desired therapeutic effect. (Tomlinson, *Nature Biotechnology* 22, 521-522 (2004)). Here, a high affinity anti-SA variant would stay in serum circulation matching that of the species' serum albumin (WO2008096158). Once in circulation, any fused therapeutic agent to the AlbuAb™ variant (an AlbuAb is an anti-serum albumin dAb or immunoglobulin single variable domain), be it NCE, peptide or protein, consequently would be able to act longer on its target and exhibit a longer lasting therapeutic effect. This would allow for targeting chronic or persistent diseases without the need of frequent dosing.

A variant with moderate affinity (but specificity to SA) would only stay in serum circulation for a short time (eg, for a few hours or a few days) allowing for the specific targeting of therapeutic targets involved in acute diseases by the fused therapeutic agent.

This way it is possible to tailor the anti-SA-containing product to the therapeutic disease area by choosing an anti-SA variant with the appropriate albumin binding affinity and/or serum half-life.

An aspect of the invention provides a multispecific ligand comprising any anti-SA variant as described above and a binding moiety that specifically binds a target antigen other than SA.

An aspect of the invention provides a fusion product, eg, a fusion protein or fusion with a peptide or NCE (new chemical entity) drug, comprising a polypeptide, protein, peptide or

NCE drug fused or conjugated (for an NCE) to any variant as described above, wherein the variant is DOM7h-14-10 (or a variant having an amino acid that is at least 95, 96, 97, 98 or 99% identical to the amino acid sequence of DOM7h-14-10). DOM7h-14-10 gives only a modest drop in affinity when fused or conjugated to partner, making it useful in fusion products.

An aspect of the invention provides a composition comprising a variant, fusion protein or ligand of any preceding aspect and a pharmaceutically acceptable diluent, carrier, excipient or vehicle.

An aspect of the invention provides a method of treating or preventing a disease or disorder in a patient, comprising administering at least one dose of a variant according to any aspect or embodiment of the invention to said patient.

An aspect of the invention provides a polypeptide fusion or conjugate comprising an anti-serum albumin dAb as disclosed herein (eg, DOM7h-14-10) and an incretin or insulinotropic agent, eg, exendin-4, GLP-1(7-37), GLP-1(6-36) or any incretin or insulinotropic agent disclosed in WO06/059106, these agents being explicitly incorporated herein by reference as though written herein for inclusion in the present invention and claims below.

#### BRIEF DESCRIPTION OF THE DRAWINGS

FIG. 1: Amino-acid sequence alignment for DOM7h-14 variant dAbs. A “.” at a particular position indicates the same amino acid as found in DOM7h-14 at that position. The CDRs are indicated by underlining and bold text (the first underlined sequence is CDR1, the second underlined sequence is CDR2 and the third underlined sequence is CDR3).

FIG. 2: Kinetic parameters of DOM7h-14 variants. KD units=nM; Kd units=sec<sup>-1</sup>; Ka units=M<sup>-1</sup> sec<sup>-1</sup>. The notation A e-B means A×10<sup>-B</sup> and C e D means C×10<sup>D</sup>. The overall kinetic ranges in various species, as supported by the examples below, are indicated. Optional ranges are also provided for use in particular therapeutic settings (acute or chronic indications, conditions or diseases and “intermediate” for use in both chronic and acute settings). High affinity dAbs and products comprising these are useful for chronic settings. Medium affinity dAbs and products comprising these are useful for intermediate settings. Low affinity dAbs and products comprising these are useful for acute settings. The affinity in this respect is the affinity for serum albumin. Various example anti-serum dAbs and fusion proteins are listed, and these support the ranges disclosed. Many of the examples have favourable kinetics in human and one or more non-human animals (eg, in human and *Cynomolgus* monkey and/or mouse). Choice of dAb or product comprising this can be tailored, according to the invention, depending on the setting (eg, chronic or acute) to be treated therapeutically.

#### DETAILED DESCRIPTION OF THE INVENTION

Within this specification the invention has been described, with reference to embodiments, in a way which enables a clear and concise specification to be written. It is intended and should be appreciated that embodiments may be variously combined or separated without parting from the invention.

Unless defined otherwise, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art (e.g., in cell culture, molecular genetics, nucleic acid chemistry, hybridization techniques and biochemistry). Standard techniques are used for molecular, genetic and biochemical methods (see generally, Sambrook et al., *Molecular Cloning: A Laboratory Manual*, 2d ed.

(1989) Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. and Ausubel et al., *Short Protocols in Molecular Biology* (1999) 4<sup>th</sup> Ed, John Wiley & Sons, Inc. which are incorporated herein by reference) and chemical methods.

As used herein, the term “antagonist of Tumor Necrosis Factor Receptor 1 (TNFR1)” or “anti-TNFR1 antagonist” or the like refers to an agent (e.g., a molecule, a compound) which binds TNFR1 and can inhibit a (i.e., one or more) function of TNFR1. For example, an antagonist of TNFR1 can inhibit the binding of TNF $\alpha$  to TNFR1 and/or inhibit signal transduction mediated through TNFR1. Accordingly, TNFR1-mediated processes and cellular responses (e.g., TNF $\alpha$ -induced cell death in a standard L929 cytotoxicity assay) can be inhibited with an antagonist of TNFR1.

A “patient” is any animal, eg, a mammal, eg, a non-human primate (such as a baboon, rhesus monkey or *Cynomolgus* monkey), mouse, human, rabbit, rat, dog, cat or pig. In one embodiment, the patient is a human.

As used herein, “peptide” refers to about two to about 50 amino acids that are joined together via peptide bonds.

As used herein, “polypeptide” refers to at least about 50 amino acids that are joined together by peptide bonds. Polypeptides generally comprise tertiary structure and fold into functional domains.

As used herein an antibody refers to IgG, IgM, IgA, IgD or IgE or a fragment (such as a Fab, F(ab')<sub>2</sub>, Fv, disulphide linked Fv, scFv, closed conformation multispecific antibody, disulphide-linked scFv, diabody) whether derived from any species naturally producing an antibody, or created by recombinant DNA technology; whether isolated from serum, B-cells, hybridomas, transfectomas, yeast or bacteria.

As used herein, “antibody format” refers to any suitable polypeptide structure in which one or more antibody variable domains can be incorporated so as to confer binding specificity for antigen on the structure. A variety of suitable antibody formats are known in the art, such as, chimeric antibodies, humanized antibodies, human antibodies, single chain antibodies, bispecific antibodies, antibody heavy chains, antibody light chains, homodimers and heterodimers of antibody heavy chains and/or light chains, antigen-binding fragments of any of the foregoing (e.g., a Fv fragment (e.g., single chain Fv (scFv), a disulfide bonded Fv), a Fab fragment, a Fab' fragment, a F(ab')<sub>2</sub> fragment), a single antibody variable domain (e.g., a dAb, V<sub>H</sub>, V<sub>HH</sub>, V<sub>L</sub>), and modified versions of any of the foregoing (e.g., modified by the covalent attachment of polyethylene glycol or other suitable polymer or a humanized V<sub>HH</sub>).

The phrase “immunoglobulin single variable domain” refers to an antibody variable domain (V<sub>H</sub>, V<sub>HH</sub>, V<sub>L</sub>) that specifically binds an antigen or epitope independently of different V regions or domains. An immunoglobulin single variable domain can be present in a format (e.g., homo- or hetero-multimer) with other variable regions or variable domains where the other regions or domains are not required for antigen binding by the single immunoglobulin variable domain (i.e., where the immunoglobulin single variable domain binds antigen independently of the additional variable domains). A “domain antibody” or “dAb” is the same as an “immunoglobulin single variable domain” as the term is used herein. A “single immunoglobulin variable domain” is the same as an “immunoglobulin single variable domain” as the term is used herein. A “single antibody variable domain” or an “antibody single variable domain” is the same as an “immunoglobulin single variable domain” as the term is used herein. An immunoglobulin single variable domain is in one embodiment a human antibody variable domain, but also includes single antibody variable domains from other species

such as rodent (for example, as disclosed in WO 00/29004, the contents of which are incorporated herein by reference in their entirety), nurse shark and Camelid  $V_{HHH}$  dAbs. Camelid  $V_{HHH}$  are immunoglobulin single variable domain polypeptides that are derived from species including camel, llama, alpaca, dromedary, and guanaco, which produce heavy chain antibodies naturally devoid of light chains. The  $V_{HHH}$  may be humanized.

A "domain" is a folded protein structure which has tertiary structure independent of the rest of the protein. Generally, domains are responsible for discrete functional properties of proteins, and in many cases may be added, removed or transferred to other proteins without loss of function of the remainder of the protein and/or of the domain. A "single antibody variable domain" is a folded polypeptide domain comprising sequences characteristic of antibody variable domains. It therefore includes complete antibody variable domains and modified variable domains, for example, in which one or more loops have been replaced by sequences which are not characteristic of antibody variable domains, or antibody variable domains which have been truncated or comprise N- or C-terminal extensions, as well as folded fragments of variable domains which retain at least the binding activity and specificity of the full-length domain.

In the instant application, the term "prevention" and "preventing" involves administration of the protective composition prior to the induction of the disease or condition. "Treatment" and "treating" involves administration of the protective composition after disease or condition symptoms become manifest. "Suppression" or "suppressing" refers to administration of the composition after an inductive event, but prior to the clinical appearance of the disease or condition.

As used herein, the term "dose" refers to the quantity of ligand administered to a subject all at one time (unit dose), or in two or more administrations over a defined time interval. For example, dose can refer to the quantity of ligand (e.g., ligand comprising an immunoglobulin single variable domain that binds target antigen) administered to a subject over the course of one day (24 hours) (daily dose), two days, one week, two weeks, three weeks or one or more months (e.g., by a single administration, or by two or more administrations). The interval between doses can be any desired amount of time. The term "pharmaceutically effective" when referring to a dose means sufficient amount of the ligand, domain or pharmaceutically active agent to provide the desired effect. The amount that is "effective" will vary from subject to subject, depending on the age and general condition of the individual, the particular drug or pharmaceutically active agent and the like. Thus, it is not always possible to specify an exact "effective" amount applicable for all patients. However, an appropriate "effective" dose in any individual case may be determined by one of ordinary skill in the art using routine experimentation.

Methods for pharmacokinetic analysis and determination of ligand (eg, single variable domain, fusion protein or multi-specific ligand) half-life will be familiar to those skilled in the art. Details may be found in Kenneth, A et al: Chemical Stability of Pharmaceuticals: A Handbook for Pharmacists and in Peters et al, Pharmacokinetic analysis: A Practical Approach (1996). Reference is also made to "Pharmacokinetics", M Gibaldi & D Perron, published by Marcel Dekker, 2<sup>nd</sup> Rev. ex edition (1982), which describes pharmacokinetic parameters such as t alpha and t beta half lives and area under the curve (AUC). Optionally, all pharmacokinetic parameters and values quoted herein are to be read as being values in a

human. Optionally, all pharmacokinetic parameters and values quoted herein are to be read as being values in a mouse or rat or *Cynomolgus* monkey.

Half lives ( $t_{1/2}$  alpha and  $t_{1/2}$  beta) and AUC can be determined from a curve of serum concentration of ligand against time. The WinNonlin analysis package, eg version 5.1 (available from Pharsight Corp., Mountain View, Calif. 94040, USA) can be used, for example, to model the curve. When two-compartment modeling is used, in a first phase (the alpha phase) the ligand is undergoing mainly distribution in the patient, with some elimination. A second phase (beta phase) is the phase when the ligand has been distributed and the serum concentration is decreasing as the ligand is cleared from the patient. The t alpha half life is the half life of the first phase and the t beta half life is the half life of the second phase. Thus, in one embodiment, in the context of the present invention, the variable domain, fusion protein or ligand has a  $t_{\alpha}$  half-life in the range of (or of about) 15 minutes or more. In one embodiment, the lower end of the range is (or is about) 30 minutes, 45 minutes, 1 hour, 2 hours, 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 10 hours, 11 hours or 12 hours. In addition, or alternatively, the variable domain, fusion protein or ligand according to the invention will have a  $t_{\alpha}$  half life in the range of up to and including 12 hours (or about 12 hours). In one embodiment, the upper end of the range is (or is about) 11, 10, 9, 8, 7, 6 or 5 hours. An example of a suitable range is (or is about) 1 to 6 hours, 2 to 5 hours or 3 to 4 hours.

In one embodiment, the present invention provides the variable domain, fusion protein or ligand according to the invention has a  $t_{\beta}$  half-life in the range of (or of about) 2.5 hours or more. In one embodiment, the lower end of the range is (or is about) 3 hours, 4 hours, 5 hours, 6 hours, 7 hours, 10 hours, 11 hours, or 12 hours. In addition, or alternatively, the  $t_{\beta}$  half-life is (or is about) up to and including 21 or 25 days. In one embodiment, the upper end of the range is (or is about) 12 hours, 24 hours, 2 days, 3 days, 5 days, 10 days, 15 days, 19 days, 20 days, 21 days or 22 days. For example, the variable domain, fusion protein or ligand according to the invention will have a  $t_{\beta}$  half life in the range 12 to 60 hours (or about 12 to 60 hours). In a further embodiment, it will be in the range 12 to 48 hours (or about 12 to 48 hours). In a further embodiment still, it will be in the range 12 to 26 hours (or about 12 to 26 hours).

As an alternative to using two-compartment modeling, the skilled person will be familiar with the use of non-compartmental modeling, which can be used to determine terminal half-lives (in this respect, the term "terminal half-life" as used herein means a terminal half-life determined using non-compartmental modeling). The WinNonlin analysis package, eg version 5.1 (available from Pharsight Corp., Mountain View, Calif. 94040, USA) can be used, for example, to model the curve in this way. In this instance, in one embodiment the single variable domain, fusion protein or ligand has a terminal half life of at least (or at least about) 8 hours, 10 hours, 12 hours, 15 hours, 28 hours, 20 hours, 1 day, 2 days, 3 days, 7 days, 14 days, 15 days, 16 days, 17 days, 18 days, 19 days, 20 days, 21 days, 22 days, 23 days, 24 days or 25 days. In one embodiment, the upper end of this range is (or is about) 24 hours, 48 hours, 60 hours or 72 hours or 120 hours. For example, the terminal half-life is (or is about) from 8 hours to 60 hours, or 8 hours to 48 hours or 12 to 120 hours, eg, in man.

In addition, or alternatively to the above criteria, the variable domain, fusion protein or ligand according to the invention has an AUC value (area under the curve) in the range of (or of about) 1 mg-min/ml or more. In one embodiment, the lower end of the range is (or is about) 5, 10, 15, 20, 30, 100, 200 or 300 mg-min/ml. In addition, or alternatively, the vari-

able domain, fusion protein or ligand according to the invention has an AUC in the range of (or of about) up to 600 mg·min/ml. In one embodiment, the upper end of the range is (or is about) 500, 400, 300, 200, 150, 100, 75 or 50 mg·min/ml. Advantageously the variable domain, fusion protein or ligand will have an AUC in (or about in) the range selected from the group consisting of the following: 15 to 150 mg·min/ml, 15 to 100 mg·min/ml, 15 to 75 mg·min/ml, and 15 to 50 mg·min/ml.

“Surface Plasmon Resonance”: Competition assays can be used to determine if a specific antigen or epitope, such as human serum albumin, competes with another antigen or epitope, such as *cynomolgus* serum albumin, for binding to a serum albumin binding ligand described herein, such as a specific dAb. Similarly competition assays can be used to determine if a first ligand such as dAb, competes with a second ligand such as a dAb for binding to a target antigen or epitope. The term “competes” as used herein refers to substance, such as a molecule, compound, preferably a protein, which is able to interfere to any extent with the specific binding interaction between two or more molecules. The phrase “does not competitively inhibit” means that substance, such as a molecule, compound, preferably a protein, does not interfere to any measurable or significant extent with the specific binding interaction between two or more molecules. The specific binding interaction between two or more molecules preferably includes the specific binding interaction between a single variable domain and its cognate partner or target. The interfering or competing molecule can be another single variable domain or it can be a molecule that is structurally and/or functionally similar to a cognate partner or target.

The term “binding moiety” refers to a domain that specifically binds an antigen or epitope independently of a different epitope or antigen binding domain. A binding moiety may be a domain antibody (dAb) or may be a domain which is a derivative of a non-immunoglobulin protein scaffold, eg, a scaffold selected from the group consisting of CTLA-4, lipocalin, SpA, an affibody, an avimer, GroEl, transferrin, GroES and fibronectin, which binds to a ligand other than the natural ligand (in the case of the present invention, the moiety binds serum albumin). See WO2008/096158, which discloses examples of protein scaffolds and methods for selecting antigen or epitope-specific binding domains from repertoires (see Examples 17 to 25). These specific disclosures of WO2008/096158 are expressly incorporated herein by reference as though explicitly written herein and for use with the present invention, and it is contemplated that any part of such disclosure can be incorporated into one or more claims herein).

In a first aspect, the invention provides an anti-serum albumin (SA) immunoglobulin single variable domain variant of DOM7h-14, wherein the variant comprises at least one mutation in CDR3 region 92 to 96 (position numbering according to Kabat) compared to DOM7h-14, and wherein the variant has from 1 to 8 changes compared to the amino acid sequence of DOM7h-14.

Optionally, the variant comprises an AQG(X1)(X2)(X3)P(X4)T motif, wherein A is at position 89 (according to Kabat), and at least one of (X1) to (X4) represents an amino acid change compared to the sequence of DOM7h-14.

In one embodiment, position 95 (according to Kabat) is Pro. Additionally or alternatively, in one embodiment position 89 (according to Kabat) is Ala. Additionally or alternatively, in one embodiment position 90 (according to Kabat) is Gln. Additionally or alternatively, in one embodiment position 91 (according to Kabat) is Gly. Additionally or alternatively, in one embodiment position 97 (according to Kabat) is Thr.

In an embodiment, the variant comprises a mutation at each of positions 92, 93 and 94 and optionally position 96 (numbering according to Kabat) compared to DOM7h-14.

Optionally, the variant comprises one or more amino acid residues selected from

Position 92=L or F,

Position 93=R, M or K,

Position 94=H or K, and

Position 96=K or M (numbering according to Kabat).

In one embodiment, the variant comprises a Lys or Met at position 96 (numbering according to Kabat) compared to DOM7h-14. In this embodiment, optionally the variant comprises one or more amino acid residues selected from

Position 92=L or F,

Position 93=R, M or K, and

Position 94=H or K (numbering according to Kabat).

In one embodiment, the variant comprises an amino acid sequence that is identical to the amino acid sequence of a single variable domain selected from DOM7h-14-10, DOM7h-14-18, DOM7h-14-28 and DOM7h-14-36 or has up to 4 changes compared to the selected amino acid sequence, wherein the variant comprises at least one mutation in CDR3 region 92 to 96 (position numbering according to Kabat) compared to DOM7h-14.

An aspect of the invention provides an anti-serum albumin (SA) binding moiety comprising CDR3 of a variant according to the first aspect of the invention. In one embodiment, the SA-binding moiety comprises CDR1 of the selected variant or an amino acid sequence that is at least 50% identical to CDR1 of the selected variant. Additionally or alternatively, in an embodiment the SA-binding moiety comprises CDR2 of the selected variant or an amino acid sequence that is at least 50% identical to CDR2 of the selected variant.

In a further aspect of the invention, there is provided an anti-serum albumin (SA) immunoglobulin single variable domain variant of DOM7h-14, wherein the variant comprises a Ser at position 22 and a Glu at position 42 (numbering according to Kabat) compared to DOM7h-14, and wherein the variant has from 0 to 4 further changes compared to the amino acid sequence of DOM7h-14. In one embodiment, the variant comprises an amino acid sequence that is identical to the amino acid sequence of DOM7h-14-19 or has up to 4 changes compared to the amino acid sequence of DOM7h-14-19, wherein the variant comprises a Ser at position 22 and a Glu at position 42 (numbering according to Kabat) compared to DOM7h-14.

In one embodiment, the variant or binding moiety according to any aspect or embodiment of the invention comprises one or more of the following kinetic characteristics:—

(a) The variant or moiety comprises a binding site that specifically binds human SA with a dissociation constant (KD) from (or from about) 0.1 to (or to about) 10000 nM, optionally from (or from about) 1 to (or to about) 6000 nM, as determined by surface plasmon resonance;

(b) The variant or moiety comprises a binding site that specifically binds human SA with an off-rate constant ( $K_{off}$ ) from (or from about)  $1.5 \times 10^{-4}$  to (or to about)  $0.1 \text{ sec}^{-1}$ , optionally from (or from about)  $3 \times 10^{-4}$  to (or to about)  $0.1 \text{ sec}^{-1}$  as determined by surface plasmon resonance;

(c) The variant or moiety comprises a binding site that specifically binds human SA with an on-rate constant ( $K_{on}$ ) from (or from about)  $2 \times 10^6$  to (or to about)  $1 \times 10^4 \text{ M}^{-1} \text{ sec}^{-1}$ , optionally from (or from about)  $1 \times 10^6$  to (or to about)  $2 \times 10^4 \text{ M}^{-1} \text{ sec}^{-1}$  as determined by surface plasmon resonance;

- (d) The variant or moiety comprises a binding site that specifically binds *Cynomolgus* monkey SA with a dissociation constant (KD) from (or from about) 0.1 to (or to about) 10000 nM, optionally from (or from about) 1 to (or to about) 6000 nM, as determined by surface plasmon resonance;
- (e) The variant or moiety of any preceding claim, wherein the variant comprises a binding site that specifically binds *Cynomolgus* monkey SA with an off-rate constant ( $K_{off}$ ) from (or from about)  $1.5 \times 10^{-4}$  to (or to about)  $0.1 \text{ sec}^{-1}$ , optionally from (or from about)  $3 \times 10^{-4}$  to (or to about)  $0.1 \text{ sec}^{-1}$  as determined by surface plasmon resonance;
- (f) The variant or moiety of any preceding claim, wherein the variant comprises a binding site that specifically binds *Cynomolgus* monkey SA with an on-rate constant ( $K_{on}$ ) from (or from about)  $2 \times 10^6$  to (or to about)  $1 \times 10^4 \text{ M}^{-1} \text{ sec}^{-1}$ , optionally from (or from about)  $1 \times 10^6$  to (or to about)  $5 \times 10^3 \text{ M}^{-1} \text{ sec}^{-1}$  as determined by surface plasmon resonance;
- (g) The variant or moiety comprises a binding site that specifically binds rat SA with a dissociation constant (KD) from (or from about) 1 to (or to about) 10000 nM, optionally from (or from about) 20 to (or to about) 6000 nM, as determined by surface plasmon resonance;
- (h) The variant or moiety comprises a binding site that specifically binds rat SA with an off-rate constant ( $K_{off}$ ) from (or from about)  $2 \times 10^{-3}$  to (or to about)  $0.15 \text{ sec}^{-1}$ , optionally from (or from about)  $9 \times 10^{-3}$  to (or to about)  $0.14 \text{ sec}^{-1}$  as determined by surface plasmon resonance;
- (i) The variant or moiety comprises a binding site that specifically binds rat SA with an on-rate constant ( $K_{on}$ ) from (or from about)  $2 \times 10^6$  to (or to about)  $1 \times 10^4 \text{ M}^{-1} \text{ sec}^{-1}$ , optionally from (or from about)  $1 \times 10^6$  to (or to about)  $3 \times 10^4 \text{ M}^{-1} \text{ sec}^{-1}$  as determined by surface plasmon resonance;
- (j) The variant or moiety comprises a binding site that specifically binds mouse SA with a dissociation constant (KD) from (or from about) 1 to (or to about) 10000 nM as determined by surface plasmon resonance;
- (k) The variant or moiety comprises a binding site that specifically binds mouse SA with an off-rate constant ( $K_{off}$ ) from (or from about)  $2 \times 10^{-3}$  to (or to about)  $0.15 \text{ sec}^{-1}$  as determined by surface plasmon resonance; and/or
- (l) The variant or moiety comprises a binding site that specifically binds mouse SA with an on-rate constant ( $K_{on}$ ) from (or from about)  $2 \times 10^6$  to (or to about)  $1 \times 10^4 \text{ M}^{-1} \text{ sec}^{-1}$ , optionally from (or from about)  $2 \times 10^6$  to (or to about)  $1.5 \times 10^4 \text{ M}^{-1} \text{ sec}^{-1}$  as determined by surface plasmon resonance.

Optionally, the variant or moiety has

- I: a KD according to (a) and (d), a  $K_{off}$  according to (b) and (e), and a  $K_{on}$  according to (c) and (f); or
- II: a KD according to (a) and (g), a  $K_{off}$  according to (b) and (h), and a  $K_{on}$  according to (c) and (i); or
- III: a KD according to (a) and (j), a  $K_{off}$  according to (b) and (k), and a  $K_{on}$  according to (c) and (l); or
- IV: kinetics according to I and II; or
- V: kinetics according to I and III; or
- VI: kinetics according to I, II and III.

The invention also provides a ligand comprising a variant or moiety of any preceding aspect or embodiment of the invention. For example, the ligand can be a dual-specific ligand (see WO04003019 for examples of dual-specific ligands). In one aspect, the invention provides a multispecific ligand comprising an anti-SA variant or moiety of any pre-

ceding aspect or embodiment of the invention and a further binding moiety that specifically binds a target antigen other than SA. The or each binding moiety can be any binding moiety that specifically binds a target, eg, the moiety is an antibody, antibody fragment, scFv, Fab, dAb or a binding moiety comprising a non-immunoglobulin protein scaffold. Such moieties are disclosed in detail in WO2008/096158 (see examples 17 to 25, which disclosure is incorporated herein by reference). Examples of non-immunoglobulin scaffolds are CTLA-4, lipocalin, staphylococcal protein A (spA), Affibody™, Avimers™, GroEL and fibronectin.

In one embodiment, a linker is provided between the anti-target binding moiety and the anti-SA single variant or moiety, the linker comprising the amino acid sequence AST, optionally ASTSGPS, eg, where anti-SA and anti-target dAbs are used. Alternative linkers are described in WO2007085814 (incorporated herein by reference) and WO2008/096158 (see the passage at page 135, line 12 to page 140, line 14, which disclosure and all sequences of linkers are expressly incorporated herein by reference as though explicitly written herein and for use with the present invention, and it is contemplated that any part of such disclosure can be incorporated into one or more claims herein).

In one embodiment of the multispecific ligand, the target antigen may be, or be part of, polypeptides, proteins or nucleic acids, which may be naturally occurring or synthetic. In this respect, the ligand of the invention may bind the target antigen and act as an antagonist or agonist (e.g., EPO receptor agonist). One skilled in the art will appreciate that the choice is large and varied. They may be for instance, human or animal proteins, cytokines, cytokine receptors, where cytokine receptors include receptors for cytokines, enzymes, co-factors for enzymes or DNA binding proteins. Suitable cytokines and growth factors include, but are preferably not limited to: ApoE, Apo-SAA, BDNF, Cardiotrophin-1, EGF, EGF receptor, ENA-78, Eotaxin, Eotaxin-2, Exodus-2, EpoR, FGF-acidic, FGF-basic, fibroblast growth factor-10, FLT3 ligand, Fractalkine (CX3C), GDNF, G-CSF, GM-CSF, GF- $\beta$ 1, insulin, IFN- $\gamma$ , IGF-1, IGF-II, IL-1 $\alpha$ , IL-1 $\beta$ , IL-2, IL-3, IL-4, IL-5, IL-6, IL-7, IL-8 (72 a.a.), IL-8 (77 a.a.), IL-9, IL-10, IL-11, IL-12, IL-13, IL-15, IL-16, IL-17, IL-18 (IGIF), Inhibin  $\alpha$ , Inhibin  $\beta$ , IP-10, keratinocyte growth factor-2 (KGF-2), KGF, Leptin, LIF, Lymphotactin, Mullerian inhibitory substance, monocyte colony inhibitory factor, monocyte attractant protein, M-CSF, MDC (67 a.a.), MDC (69 a.a.), MCP-1 (MCAF), MCP-2, MCP-3, MCP-4, MDC (67 a.a.), MDC (69 a.a.), MIG, MIP-1 $\alpha$ , MIP-1 $\beta$ , MIP-3 $\alpha$ , MIP-3 $\beta$ , MIP-4, myeloid progenitor inhibitor factor-1 (MPlF-1), NAP-2, Neurturin, Nerve growth factor,  $\beta$ -NGF, NT-3, NT-4, Oncostatin M, PDGF-AA, PDGF-AB, PDGF-BB, PF-4, RANTES, SDF1 $\alpha$ , SDF1 $\beta$ , SCF, SCGF, stem cell factor (SCF), TARC, TGF- $\alpha$ , TGF- $\beta$ , TGF- $\beta$ 2, TGF- $\beta$ 3, tumour necrosis factor (TNF), TNF- $\alpha$ , TNF- $\beta$ , TNF receptor I, TNF receptor II, TNIL-1, TPO, VEGF, VEGF receptor 1, VEGF receptor 2, VEGF receptor 3, GCP-2, GRO/MGSA, GRO- $\beta$ , GRO- $\gamma$ , HCC1, 1-309, HER 1, HER 2, HER 3 and HER 4, CD4, human chemokine receptors CXCR4 or CCR5, non-structural protein type 3 (NS3) from the hepatitis C virus, TNF-alpha, IgE, IFN-gamma, MMP-12, CEA, *H. pylori*, TB, influenza, Hepatitis E, MMP-12, internalizing receptors that are over-expressed on certain cells, such as the epidermal growth factor receptor (EGFR), ErbB2 receptor on tumor cells, an internalising cellular receptor, LDL receptor, FGF2 receptor, ErbB2 receptor, transferrin receptor, PDGF receptor, VEGF receptor, PsmAr, an extracellular matrix protein, elastin, fibronectin, laminin,  $\alpha$ 1-antitrypsin, tissue factor protease inhibitor, PDK1, GSK1, Bad, caspase-9, Forkhead, an

antigen of *Helicobacter pylori*, an antigen of *Mycobacterium tuberculosis*, and an antigen of influenza virus. It will be appreciated that this list is by no means exhaustive.

In one embodiment, the multispecific ligand comprises an anti-SA dAb variant or moiety of the invention and an anti-TNFR1 binding moiety, eg, an anti-TNFR1 dAb. Optionally, the ligand has only one anti-TNFR1 binding moiety (eg, dAb) to reduce the chance of receptor cross-linking. In one embodiment, the anti-SA dAb variant is DOM7h-14-10.

In one embodiment, the anti-TNFR1 binding moiety is DOM1h-131-206 disclosed in WO2008149148 (the amino acid sequence of which and the nucleotide sequence of which, as disclosed in that PCT application, are expressly incorporated herein by reference as though explicitly written herein and for use with the present invention, and it is contemplated that any part of such disclosure can be incorporated into one or more claims herein). In one embodiment, the multispecific ligand comprises or consists of the amino acid sequence of DOM1h-131-206 and the amino acid sequence of DOM7h-14-10.

In one embodiment, the anti-TNFR1 binding moiety or dAb is any such moiety or dAb disclosed in co-pending application U.S. Ser. No. 61/153,746, the disclosure of which is incorporated herein by reference. In one embodiment, the anti-TNFR1 binding moiety comprises an amino acid sequence that is at least 95% identical to the amino acid sequence of DOM1h-574-156, DOM1h-574-72, DOM1h-574-109, DOM1h-574-138, DOM1h-574-162 or DOM1h-574-180 or the amino acid sequence of any anti-TNFR1 dAb disclosed in Table 3. In one embodiment, the multispecific ligand comprises or consists of the amino acid sequence of DOM1h-574-156 and the amino acid sequence of DOM7h-14-10.

In one embodiment, the ligand of the invention is a fusion protein comprising a variant or moiety of the invention fused directly or indirectly to one or more polypeptides. For example, the fusion protein can be a "drug fusion" as disclosed in WO2005/118642 (the disclosure of which is incorporated herein by reference), comprising a variant or moiety of the invention and a polypeptide drug as defined in that PCT application.

As used herein, "drug" refers to any compound (e.g., small organic molecule, nucleic acid, polypeptide) that can be administered to an individual to produce a beneficial, therapeutic or diagnostic effect through binding to and/or altering the function of a biological target molecule in the individual. The target molecule can be an endogenous target molecule encoded by the individual's genome (e.g. an enzyme, receptor, growth factor, cytokine encoded by the individual's genome) or an exogenous target molecule encoded by the genome of a pathogen (e.g. an enzyme encoded by the genome of a virus, bacterium, fungus, nematode or other pathogen). Suitable drugs for use in fusion proteins and conjugates comprising an anti-SA dAb variant of the invention are disclosed in WO2005/118642 and WO2006/059106 (the entire disclosures of which are incorporated herein by reference, and including the entire list of specific drugs as though this list were expressly written herein, and it is contemplated that such incorporation provides disclosure of specific drugs for inclusion in claims herein). For example, the drug can be glucagon-like peptide 1 (GLP-1) or a variant, interferon alpha 2b or a variant or extendin-4 or a variant.

In one embodiment, the invention provides a drug conjugate as defined and disclosed in WO2005/118642 and WO2006/059106, wherein the conjugate comprises a variant or moiety of the invention. In one example, the drug is covalently linked to the variant or moiety (eg, the variant or

moiety and the drug are expressed as part of a single polypeptide). Alternatively, in an example, the drug is non-covalently bonded or associated with the variant or moiety. The drug can be covalently or noncovalently bonded to the variant or moiety directly or indirectly (e.g., through a suitable linker and/or noncovalent binding of complementary binding partners (e.g., biotin and avidin)). When complementary binding partners are employed, one of the binding partners can be covalently bonded to the drug directly or through a suitable linker moiety, and the complementary binding partner can be covalently bonded to the variant or moiety directly or through a suitable linker moiety. When the drug is a polypeptide or peptide, the drug composition can be a fusion protein, wherein the polypeptide or peptide, drug and the polypeptide binding moiety are discrete parts (moieties) of a continuous polypeptide chain. As described herein, the polypeptide binding moieties and polypeptide drug moieties can be directly bonded to each other through a peptide bond, or linked through a suitable amino acid, or peptide or polypeptide linker.

A ligand which contains one single variable domain (monomer) variant or moiety of the invention or more than one single variable domain or moiety (multimer, fusion protein, conjugate, and dual specific ligand as defined herein) which specifically binds to serum albumin, can further comprise one or more entities selected from, but preferably not limited to a label, a tag, an additional single variable domain, a dAb, an antibody, an antibody fragment, a marker and a drug. One or more of these entities can be located at either the COOH terminus or at the N terminus or at both the N terminus and the COOH terminus of the ligand comprising the single variable domain or moiety, (either immunoglobulin or non-immunoglobulin single variable domain). One or more of these entities can be located at either the COOH terminus, or the N terminus, or both the N terminus and the COOH terminus of the single variable domain or moiety which specifically binds serum albumin of the ligand which contains one single variable domain (monomer) or moiety or more than one single variable domains or moieties (multimer, fusion protein, conjugate, and dual specific ligand as defined herein). Non-limiting examples of tags which can be positioned at one or both of these termini include a HA, his or a myc tag. The entities, including one or more tags, labels and drugs, can be bound to the ligand which contains one single variable domain (monomer) or more than one single variable domain or moiety (multimer, fusion protein, conjugate, and dual specific ligand as defined herein), which binds serum albumin, either directly or through linkers as described above.

An aspect of the invention provides a fusion product, eg, a fusion protein or fusion with a peptide or conjugate with an NCE (new chemical entity) drug, comprising a polypeptide drug fused or conjugated (for an NCE) to any variant or moiety as described above, optionally wherein the variant or moiety is DOM7h-14-10 (or a variant having an amino acid that is at least 95, 96, 97, 98 or 99% identical to the amino acid sequence of DOM7h-14-10). DOM7h-14-10 gives only a modest drop in affinity when fused or conjugated to partner, making them useful in fusion products.

The invention provides a composition comprising a variant, fusion protein, conjugate or ligand of any aspect of the invention and a pharmaceutically acceptable diluent, carrier, excipient or vehicle.

Also encompassed herein is an isolated nucleic acid encoding any of the variants, moieties, fusion proteins, conjugates or ligands described herein, e.g., a ligand which contains one single variable domain (monomer) variant of the invention or more than one single variable domain (e.g., multimer, fusion

protein, conjugate, and dual specific ligand as defined herein) variant which specifically binds to serum albumin, or which specifically binds both human serum albumin and at least one non-human serum albumin, or functionally active fragments thereof. Also encompassed herein is a vector and/or an expression vector, a host cell comprising the vector, e.g., a plant or animal cell and/or cell line transformed with a vector, a method of expressing and/or producing one or more variants, moieties, fusion proteins or ligands which contains one single variable domain (monomer) variant or moiety or more than one single variable domain variants or moieties (e.g., multimer, fusion protein, conjugate, and dual specific ligand as defined herein) which specifically binds to serum albumin, or fragment(s) thereof encoded by said vectors, including in some instances culturing the host cell so that the one or more variants, moieties, fusion proteins or ligands or fragments thereof are expressed and optionally recovering the ligand which contains one single variable domain or moiety (monomer) or more than one single variable domain or moiety (e.g., multimer, fusion protein, conjugate, and dual specific ligand as defined herein) which specifically binds to serum albumin, from the host cell culture medium. Also encompassed are methods of contacting a ligand described herein with serum albumin, including serum albumin and/or non-human serum albumin(s), and/or one or more targets other than serum albumin, where the targets include biologically active molecules, and include animal proteins, cytokines as listed above, and include methods where the contacting is in vitro as well as administering any of the variants, moieties, fusion proteins or ligands described herein to an individual host animal or cell in vivo and/or ex vivo. Preferably, administering ligands described herein which comprises a single variable domain (immunoglobulin or non-immunoglobulin) directed to serum albumin and/or non-human serum albumin(s), and one or more domains directed to one or more targets other than serum albumin, will increase the half life, including the T beta and/or terminal half life, of the anti-target ligand. Nucleic acid molecules encoding the variants, fusion proteins or single domain containing ligands or fragments thereof, including functional fragments thereof, are contemplated herein. Vectors encoding the nucleic acid molecules, including but preferably not limited to expression vectors, are contemplated herein, as are host cells from a cell line or organism containing one or more of these expression vectors. Also contemplated are methods of producing any variant, fusion protein or ligand, including, but preferably not limited to any of the aforementioned nucleic acids, vectors and host cells.

An aspect of the invention provides a nucleic acid comprising a nucleotide sequence encoding a variant according to the invention or a multispecific ligand of the invention or fusion protein of the invention.

An aspect of the invention provides a nucleic acid comprising the nucleotide sequence of a DOM7h-14 variant selected from DOM7h-14-10, DOM7h-14-18, DOM7h-14-28, DOM7h-14-36 and DOM7h-14-19 or a nucleotide sequence that is at least 70, 75, 80, 85, 90, 95, 96, 97, 98 or 99% identical to said selected sequence.

An aspect of the invention provides a vector comprising the nucleic acid of the invention. An aspect of the invention provides an isolated host cell comprising the vector.

Reference is made to WO2008/096158 for details of library vector systems, combining single variable domains, characterization of dual specific ligands, structure of dual specific ligands, scaffolds for use in constructing dual specific ligands, uses of anti-serum albumin dAbs and multispecific ligands and half-life-enhanced ligands, and compositions and formulations of comprising anti-serum albumin dAbs. These

disclosures are incorporated herein by reference to provide guidance for use with the present invention, including for variants, moieties, ligands, fusion proteins, conjugates, nucleic acids, vectors, hosts and compositions of the present invention.

DOM7h-11 variant sequences, which are not according to the invention, are disclosed in a co-pending US provisional patent application entitled IMPROVED ANTI-SERUM ALBUMIN BINDING VARIANTS, filed on the same day as the present application. These sequences of DOM7h-11 variants (SEQ ID NO:s 1-10 in the co-pending application) are incorporated herein by reference as though explicitly written herein.

Sequences

TABLE 1

Amino Acid Sequences of DOM7h-14 Variant dAbs	
DOM7h-14-10 (SEQ ID NO: 1)	DIQMTQSPSSLSASVGDRTITCRASQWIGSLSWYQQKPKGKAPKLLI
	MWRSSLQSGVPSRFRSGSGSGTDFTLTISLQPEDFATYYCAQGLRHPK
	TFGQGTKVEIKR
DOM7h-14-18 (SEQ ID NO: 2)	DIQMTQSPSSLSASVGDRTITCRASQWIGSLSWYQQKPKGKAPKLLIM
	WRSSLQSGVPSRFRSGSGSGTDFTLTISLQPEDFATYYCAQGLMKPMT
	FGQGTKVEIKR
DOM7h-14-19 (SEQ ID NO: 3)	DIQMTQSPSSLSASVGDRTITCRASQWIGSLSWYQQKPGEAPKLLIM
	WRSSLQSGVPSRFRSGSGSGTDFTLTISLQPEDFATYYCAQGAALPRT
	FGQGTKVEIKR
DOM7h-14-28 (SEQ ID NO: 4)	DIQMTQSPSSLSASVGDRTITCRASQWIGSLSWYQQKPKGKAPKLLIM
	WRSSLQSGVPSRFRSGSGSGTDFTLTISLQPEDFATYYCAQGAALPKT
	FGQGTKVEIKR
DOM7h-14-36 (SEQ ID NO: 5)	DIQMTQSPSSLSASVGDRTITCRASQWIGSLSWYQQKPKGKAPKLLIM
	WRSSLQSGVPSRFRSGSGSGTDFTLTISLQPEDFATYYCAQGFKKPRT
	FGQGTKVEIKR

TABLE 2

Nucleotide Sequences of DOM7h-14 Variant dAbs	
DOM7h-14-10 (SEQ ID NO: 6)	GACATCCAGA TGACCCAGTC TCCATCTCC CTGTCTGCAT
	CTGTAGGAGA CCGTGT CACC ATCACTGCC GGGCAAGTCA
	GTGGATTGGG TCTCAGTTAT CTTGGTACCA GC AGAAACCA
	GGGAAAGCCC CTAAGCTCCT GATCATGTGG CGTTCCTCGT
	TGCAAAGT GG GGTCCCATCA CGTTTCAGTG GCAGTGGATC
	TGGGACAGAT TCACTCTCA CCAT CAGCAG TCTGCAACCT
	GAAGATTTTG CTACGTACTA CTGTGCTCAG GGTTCGAGGC
	ATCCTAAGAC GTTCGGCCAA GGGACCAAGG TGGAAATCAA ACGG

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TABLE 2-continued

Nucleotide Sequences of DOM7h-14 Variant dAbs	
DOM7h-14-18 (SEQ ID NO: 7)	
GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT	
CTGTAGGAGA CCGTGT CACC ATCACTTGCC GGGCAAGTCA	
GTGGATTGGG TCTCAGTTAT CTTGGTACCA GC AGAAACCA	
GGGAAAGCCC CTAAGCTCCT GATCATGTGG CGTTCCTCGT	
TGCAAAGT GG GGTCCCATCA CGTTTCAGTG GCAGTGGATC	
TGGGACAGAT TTCACTCTCA CCAT CAGCAG TCTGCAACCT	
GAAGATTTTG CTACGTACTA CTGTGCTCAG GGTCTTATGA	
AGCCTATGAC GTTCGGCCAA GGGACCAAGG TGGAAATCAA ACGG	
DOM7h-14-19 (SEQ ID NO: 8)	
GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT	
CTGTAGGAGA CCGTGT CACC ATCTCTTGCC GGGCAAGTCA	
GTGGATTGGG TCTCAGTTAT CTTGGTACCA GC AGAAACCA	
GGGAAAGCCC CTAAGCTCCT GATCATGTGG CGTTCCTCGT	
TGCAAAGT GG GGTCCCATCA CGTTTCAGTG GCAGTGGATC	
TGGGACAGAT TTCACTCTCA CCAT CAGCAG TCTGCAACCT	
GAAGATTTTG CTACGTACTA CTGTGCTCAG GGTGCGGCGT	
TGCCTAGGAC GTTCGGCCAA GGGACCAAGG TGGAAATCAA ACGG	

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TABLE 2-continued

Nucleotide Sequences of DOM7h-14 Variant dAbs	
DOM7h-14-28 (SEQ ID NO: 9)	
5 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT	
CTGTAGGAGA CCGTGT CACC ATCACTTGCC GGGCAAGTCA	
GTGGATTGGG TCTCAGTTAT CTTGGTACCA GC AGAAACCA	
GGGAAAGCCC CTAAGCTCCT GATCATGTGG CGTTCCTCGT	10
TGCAAAGT GG GGTCCCATCA CGTTTCAGTG GCAGTGGATC	
TGGGACAGAT TTCACTCTCA CCAT CAGCAG TCTGCAACCT	
GAAGATTTTG CTACATACTA CTGTGCTCAG GGTGCGGCGT	15
TGCCTAAGAC GTTCGGCCAA GGGACCAAGG TGGAAATCAA ACGG	
DOM7h-14-36 (SEQ ID NO: 10)	
5 GACATCCAGA TGACCCAGTC TCCATCCTCC CTGTCTGCAT	
CTGTAGGAGA CCGTGT CACC ATCACTTGCC GGGCAAGTCA	20
GTGGATTGGG TCTCAGTTAT CTTGGTACCA GC AGAAACCA	
GGGAAAGCCC CTAAGCTCCT GATCATGTGG CGTTCCTCGT	
25 TGCAAAGT GG GGTCCCATCA CGTTTCAGTG GCAGTGGATC	
TGGGACAGAT TTCACTCTCA CCAT CAGCAG TCTGCAACCT	
GAAGATTTTG CTACGTACTA CTGTGCTCAG GGTTTTAAAGA	
30 AGCCTCGGAC GTTCGGCCAA GGGACCAAGG TGGAAATCAA ACGG	

TABLE 3

Amino Acid Sequences of anti-TNFR1 dAbs	
>DOM1h-509 (SEQ ID NO: 11)	
EVQLLESGGGLVQPGGSLRLSCAASGFTFSQYRMHWVRQAPGKLEWVSSIDTRGSST	
YYADPVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKAVTMFSPFFDYWGQGLTV	
TVSS	
>DOM1h-510 (SEQ ID NO: 12)	
EVQLLESGGGLVQPGGSLRLSCAASGFTFADYGMRWVRQAPGKLEWVSSITRTRGV	
YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKWRNRHGEYLADFDYWGQG	
TLVTVSS	
>DOM1h-543 (SEQ ID NO: 13)	
EVQLLESGGGLVQPGGSLRLSCAASGFTFMRYRMHWVRQAPGKLEWVSSIDSNGSST	
YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKDRTERSPPFDYWGQGLTV	
TVSS	
>DOM1h-549 (SEQ ID NO: 14)	
EVQLLESGGGLVQPGGSLRLSCAASGFTFVDYEMHWVRQAPGKLEWVSSISESGTTT	
YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKRRFSASTFDYWGQGLTV	
VSS	
>DOM1h-574 (SEQ ID NO: 15)	
EVQLLESGGGLVQPGGSLRLSCAASGFTFVKYSMGWVRQAPGKLEWVSSQISNTGGHT	
YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKYTGHWEPFDYWGQGLTV	
VSS	

TABLE 3-continued

## Amino Acid Sequences of anti-TNFR1 dAbs

>DOM1h-574-1 (SEQ ID NO: 16)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTGGHT  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKYTGRWEPDYWGQGLVT  
 VSS

>DOM1h-574-2 (SEQ ID NO: 17)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTGGHT  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKYTGRWEPFDYWGQGLVT  
 VSS

>DOM1h-574-7 (SEQ ID NO: 18)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTGGHT  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFDYWGQGLVT  
 VSS

>DOM1h-574-8 (SEQ ID NO: 19)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGPWVSQISNTGGHT  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFDYWGQGLVT  
 VSS

>DOM1h-574-9 (SEQ ID NO: 20)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTGGHT  
 YYADSVKGRFTISRDN SKNTLYMQMNSLRAEDTAVYYCAIYTGRWEPFDYWGQGLVT  
 VSS

>DOM1h-574-10 (SEQ ID NO: 21)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFGKYSMGWVRQAPGKDEWVSQISNTGGHT  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFDYWGQGLVT  
 VSS

>DOM1h-574-11 (SEQ ID NO: 22)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTGGHT  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKYTGRWEPFDHWGQGLVT  
 VSS

>DOM1h-574-12 (SEQ ID NO: 23)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTGDHT  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKYTGRWEPFDYWGQGLVT  
 VSS

>DOM1h-574-13 (SEQ ID NO: 24)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTGDRT  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAKYTGRWEPFDYWGQGLVT  
 VSS

>DOM1h-574-14 (SEQ ID NO: 25)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTGDRT  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFDYWGQGLVT  
 VSS

>DOM1h-574-15 (SEQ ID NO: 26)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTGDHT  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFDYWGQGLVT  
 VSS

TABLE 3-continued

## Amino Acid Sequences of anti-TNFR1 dAbs

>DOM1h-574-16 (SEQ ID NO: 27)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGPWWVSQISNTGDRT  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFDYWGGTLVT  
 VSS

>DOM1h-574-17 (SEQ ID NO: 28)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGPWWVSQISNTGDHT  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFDYWGGTLVT  
 VSS

>DOM1h-574-18 (SEQ ID NO: 29)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFGKYSMGWVRQAPGKDEWVSQISNTGDRT  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFDYWGGTLVT  
 VSS

>DOM1h-574-19 (SEQ ID NO: 30)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKDEWVSQISNTGDHT  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFDYWGGTLVT  
 VSS

>DOM1h-574-25 (SEQ ID NO: 31)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKLEWVSQISNTGDRT  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFVYWGGTLVT  
 VSS

>DOM1h-574-26 (SEQ ID NO: 32)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKLEWVSQISNTGDRT  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFEYWGGTLVT  
 VSS

>DOM1h-574-27 (SEQ ID NO: 33)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKLEWVSQISNTGDRT  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWKPFEYWGGTLVT  
 VSS

>DOM1h-574-28 (SEQ ID NO: 34)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKLEWVSQISNTGDRT  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWVPPFEYWGGTLVT  
 VSS

>DOM1h-574-29 (SEQ ID NO: 35)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKLEWVSQISNTGDRT  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWRPFEYWGGTLVT  
 VSS

>DOM1h-574-30 (SEQ ID NO: 36)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKLEWVSQIANTGDRR  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAAYYCAIYTGRWEPFDYWGGTLVT  
 VSS

>DOM1h-574-31 (SEQ ID NO: 37)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKLEWVSQISNTADRT  
 YYAHSVKGRTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFNYWGGTLVT  
 VSS

TABLE 3-continued

Amino Acid Sequences of anti-TNFR1 dAbs
>DOM1h-574-32 (SEQ ID NO: 38) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTGDRT  YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPPEYWGQGLT VSS
>DOM1h-574-33 (SEQ ID NO: 39) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTGDRT  YYADSVKGRFTISRDN SKNSLYLQMNSLRAEDTAVYYCAIYTGRWVPPDNWGQGLT VSS
>DOM1h-574-35 (SEQ ID NO: 40) EVQLLESGGGLVQPGGSLRRLSCAASGFTFTY SMGWVRQAPGKGLEWVSQISNTGDRT  YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPQYWGQGLT VSS
>DOM1h-574-36 (SEQ ID NO: 41) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTGDRT  YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFDYWGQGLT VSS
>DOM1h-574-37 (SEQ ID NO: 42) EVQLLESGGGLVQPGGSLRRLSCAASGFTFFKY SMGWVRQAPGKGLEWVSQISNTGDRT  YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFDYWGQGLT VSS
>DOM1h-574-38 (SEQ ID NO: 43) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTGDRR  YYDDSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFDYWGQGLT VSS
>DOM1h-574-39 (SEQ ID NO: 44) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTGDRR  YYADAVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFDYWGQGLT VSS
>DOM1h-574-40 (SEQ ID NO: 45) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTGDRT  YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFKYWGQGLT VSS
>DOM1h-574-53 (SEQ ID NO: 46) EVQLLESGGGLVQPGGSLRRLSCAASGFTFSKY SMGWVRQAPGKGLEWVSQISNTGERR  YYADSVKGRFTISRDN PKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPPEYWGQGLT VSS
>DOM1h-574-54 (SEQ ID NO: 47) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVNYS MGWVRQAPGKGLEWVSQISNTGDRT  YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPYEWYWGQGLT VTS
>DOM1h-574-65 (SEQ ID NO: 48) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQIANTGDRR  YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFVYWGQGLT VSS

TABLE 3-continued

## Amino Acid Sequences of anti-TNFR1 dAbs

>DOM1h-574-66 (SEQ ID NO: 49)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQIANTGDRR  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWKPFPEYWGQGLVT  
 VSS

>DOM1h-574-67 (SEQ ID NO: 50)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQIANTGDRR  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWVPPFEYWGQGLVT  
 VSS

>DOM1h-574-68 (SEQ ID NO: 51)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQIANTGDRR  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWRPPEYWGQGLVT  
 VSS

>DOM1h-574-69 (SEQ ID NO: 52)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQIANTGDRR  
 YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPPEYWGQGLVT  
 VSS

>DOM1h-574-70 (SEQ ID NO: 53)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTADRT  
 YYAHSVKGRTISRDN SKNTLYLQMNSLRAEDTAVYYCAVYTGRWEPFVYWGQGLVT  
 VSS

>DOM1h-574-71 (SEQ ID NO: 54)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTADRT  
 YYAHSVKGRTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWKPFPEYWGQGLVT  
 VSS

>DOM1h-574-72 (SEQ ID NO: 55)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTADRT  
 YYAHSVKGRTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWVPPFEYWGQGLVT  
 VSS

>DOM1h-574-73 (SEQ ID NO: 56)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTADRT  
 YYAHSVKGRTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWRPPEYWGQGLVT  
 VSS

>DOM1h-574-74 (SEQ ID NO: 57)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTADRT  
 YYAHSVKGRTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPPEYWGQGLVT  
 VSS

>DOM1h-574-75 (SEQ ID NO: 58)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTGDRR  
 YYDHSVKGRTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFVYWGQGLVT  
 VSS

>DOM1h-574-76 (SEQ ID NO: 59)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTGDRR  
 YYDHSVKGRTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWKPFPEYWGQGLVT  
 VSS

TABLE 3-continued

Amino Acid Sequences of anti-TNFR1 dAbs
>DOM1h-574-77 (SEQ ID NO: 60) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTGDRR  YYDHSVKGGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWV PFEYWGQGLVT  VSS
>DOM1h-574-78 (SEQ ID NO: 61) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTGDRR  YYDHSVKGGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWR PFEYWGQGLVT  VSS
>DOM1h-574-79 (SEQ ID NO: 62) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTGDRR  YYDHSVKGGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWAPFEYWGQGLVT  VSS
>DOM1h-574-84 (SEQ ID NO: 63) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTGDRR  YYADAVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWEPFVYWGQGLVT  VSS
>DOM1h-574-85 (SEQ ID NO: 64) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTGDRR  YYADAVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWKPFEYWGQGLVT  VSS
>DOM1h-574-86 (SEQ ID NO: 65) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTGDRR  YYADAVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWV PFEYWGQGLVT  VSS
>DOM1h-574-87 (SEQ ID NO: 66) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTGDRR  YYADAVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWR PFEYWGQGLVT  VSS
>DOM1h-574-88 (SEQ ID NO: 67) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTGDRR  YYADAVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWAPFEYWGQGLVT  VSS
>DOM1h-574-90 (SEQ ID NO: 68) EVQLLESGGGLVQPGGSLRRLSCAASGFTFLKFSMGWVRQAPGKGLEWVSQIANTGDRR  YYADSVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWAPFEYWGQGLVT  VSS
>DOM1h-574-91 (SEQ ID NO: 69) EVQLLESGGGLVQPGGSLRRLSCAASGFTFLKYSMGWVRQAPGKGLEWVSQISNTADRT  YYAHSVKGGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWAPFEYWGQGLVT  VSS
>DOM1h-574-92 (SEQ ID NO: 70) EVQLLESGGGLVQPGGSLRRLSCAASGFTFFKYSMGWVRQAPGKGLEWVSQISDTGDRR  YYDHSVKGGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWEPFVYWGQGLVT  VSS

TABLE 3-continued

## Amino Acid Sequences of anti-TNFR1 dAbs

>DOM1h-574-93 (SEQ ID NO: 71)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFLKYSMGWVRQAPGKGLEWVSQISDTGDRR  
YYDSSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFVYWGQGLVT  
VSS

>DOM1h-574-94 (SEQ ID NO: 72)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQIANTGDRR  
YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAAYYCAIYTGRWPDFDYWGQGLVT  
VSS

>DOM1h-574-95 (SEQ ID NO: 73)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQIANTGDRR  
YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAAYYCAIYTGRWPDFEYWGQGLVT  
VSS

>DOM1h-574-96 (SEQ ID NO: 74)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTADRT  
YYAHSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWPDFDYWGQGLVT  
VSS

>DOM1h-574-97 (SEQ ID NO: 75)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTADRT  
YYAHSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWPDFEYWGQGLVT  
VSS

>DOM1h-574-98 (SEQ ID NO: 76)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTGDRR  
YYDSSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWPDFDYWGQGLVT  
VSS

>DOM1h-574-99 (SEQ ID NO: 77)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTGDRR  
YYDSSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWPDFEYWGQGLVT  
VSS

>DOM1h-574-100 (SEQ ID NO: 78)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGP EWVSQISAWGDRR  
YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFDYWGQGLVT  
VSS

>DOM1h-574-101 (SEQ ID NO: 79)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGP EWVSQISDGGQRT  
YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFDYWGQGLVT  
VSS

>DOM1h-574-102 (SEQ ID NO: 80)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGP EWVSQISDSGYRT  
YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFDYWGQGLVT  
VSS

>DOM1h-574-103 (SEQ ID NO: 81)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGP EWVSQISDGGTRT  
YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFDYWGQGLVT  
VSS

TABLE 3-continued

Amino Acid Sequences of anti-TNFR1 dAbs
>DOM1h-574-104 (SEQ ID NO: 82) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGP EWVSQISDKGTRT  YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFDYWGQGLVT  VSS
>DOM1h-574-105 (SEQ ID NO: 83) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGP EWVSQISETGRRT  YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFDYWGQGLVT  VSS
>DOM1h-574-106 (SEQ ID NO: 84) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQIINNTGSTT  YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFDYWGQGLVT  VSS
>DOM1h-574-107 (SEQ ID NO: 85) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGP EWVSQISNTADRT  YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWVPEYWGQGLVT  VSS
>DOM1h-574-108 (SEQ ID NO: 86) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGP EWVSQISNTADRT  YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPPEYWGQGLVT  VSS
>DOM1h-574-109 (SEQ ID NO: 87) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTADRT  YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWVPEYWGQGLVT  VSS
>DOM1h-574-110 (SEQ ID NO: 88) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTADRT  YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPPEYWGQGLVT  VSS
>DOM1h-574-111 (SEQ ID NO: 89) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTADRT  YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWRPPEYWGQGLVT  VSS
>DOM1h-574-112 (SEQ ID NO: 90) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTADRT  YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPPEYWGQGLVT  VSS
>DOM1h-574-113 (SEQ ID NO: 91) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTADRR  YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPPEYWGQGLVT  VSS
>DOM1h-574-114 (SEQ ID NO: 92) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQILNTADRT  YYADSVKGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPPEYWGQGLVT  VSS

TABLE 3-continued

## Amino Acid Sequences of anti-TNFR1 dAbs

>DOM1h-574-115 (SEQ ID NO: 93)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTADRT  
 YYDHSVKGKRFITSRDNSKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPFEYWGQGLT  
 VSS

>DOM1h-574-116 (SEQ ID NO: 94)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTADRR  
 YYAHSVKGKRFITSRDNSKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPFEYWGQGLT  
 VSS

>DOM1h-574-117 (SEQ ID NO: 95)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTADRR  
 YYDHSVKGKRFITSRDNSKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPFEYWGQGLT  
 VSS

>DOM1h-574-118 (SEQ ID NO: 96)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTADRT  
 YYAHSVKGKRFITSRDNSKNTLYLQMNSLRAEDTAVYYCAVYTGWRVSPFEYWGQGLT  
 VSS

>DOM1h-574-119 (SEQ ID NO: 97)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTADRT  
 YYAHSVKGKRFITSRDNSKNTLYLQMNSLRAEDTAVYYCALYTGWRVSPFEYWGQGLT  
 VSS

>DOM1h-574-120 (SEQ ID NO: 98)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTADRT  
 YYAHSVKGKRFITSRDNSKNTLYLQMNSLRAEDTAVYYCAVYTGWRVSPFEYWGQGLT  
 VSS

>DOM1h-574-121 (SEQ ID NO: 99)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTADRT  
 YYAHSVKGKRFITSRDNSKNTLYLQMNSLRAEDTAVYYCALYTGWRVSPFEYWGQGLT  
 VSS

>DOM1h-574-122 (SEQ ID NO: 100)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQIANTADRR  
 YYAHSVKGKRFITSRDNSKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPFEYWGQGLT  
 VSS

>DOM1h-574-123 (SEQ ID NO: 101)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTADRR  
 YYADAVKGRFITSRDNSKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFVYWGQGLT  
 VSS

>DOM1h-574-124 (SEQ ID NO: 102)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTGDRR  
 YYAHAVKGRFITSRDNSKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFVYWGQGLT  
 VSS

>DOM1h-574-125 (SEQ ID NO: 103)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQIANTADRR  
 YYADAVKGRFITSRDNSKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFVYWGQGLT  
 VSS

TABLE 3-continued

Amino Acid Sequences of anti-TNFR1 dAbs
>DOM1h-574-126 (SEQ ID NO: 104) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQIANTGDRR  YYAHAVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWEPFVYWGQGLVT  VSS
>DOM1h-574-127 (SEQ ID NO: 105) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISNTADRR  YYAHAVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWEPFVYWGQGLVT  VSS
>DOM1h-574-128 (SEQ ID NO: 106) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQIANTADRR  YYAHAVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWEPFVYWGQGLVT  VSS
>DOM1h-574-129 (SEQ ID NO: 107) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQIVNTGDRR  YYADAVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWEPFVYWGQGLVT  VSS
>DOM1h-574-130 (SEQ ID NO: 108) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQIANTGDRR  YYADAVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWEPFVYWGQGLVT  VSS
>DOM1h-574-131 (SEQ ID NO: 109) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTADRT  YYDHSV KGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWAPPEYWGQGLVT  VSS
>DOM1h-574-132 (SEQ ID NO: 110) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTADRT  YYDHSV KGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWRPPEYWGQGLVT  VSS
>DOM1h-574-133 (SEQ ID NO: 111) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTADRT  YYDHSV KGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWEPFVYWGQGLVT  VSS
>DOM1h-574-134 (SEQ ID NO: 112) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTADRT  YYSHSV KGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWVPPPEYWGQGLVT  VSS
>DOM1h-574-135 (SEQ ID NO: 113) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTADRT  YYTHSV KGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWVPPPEYWGQGLVT  VSS
>DOM1h-574-137 (SEQ ID NO: 114) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTADRT  YYTDAVKGRFTISRDN SKNTLYLQMN SLRAEDTAVYYCAIYTGRWEPFVYWGQGLVT  VSS

TABLE 3-continued

## Amino Acid Sequences of anti-TNFR1 dAbs

>DOM1h-574-138 (SEQ ID NO: 115)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFFKYSMGWVRQAPGKGLEWVSIADTADRR  
 YYAHSVKGKRFITSRDNSKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPFEYWGQGLT  
 VSS

>DOM1h-574-139 (SEQ ID NO: 116)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFLKYSMGWVRQAPGKGLEWVSIADTADRR  
 YYAHSVKGKRFITSRDNSKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPFEYWGQGLT  
 VSS

>DOM1h-574-140 (SEQ ID NO: 117)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFFKYSMGWVRQAPGKGLEWVSIADTADRR  
 YYDHSVKGKRFITSRDNSKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFVYWGQGLT  
 VSS

>DOM1h-574-141 (SEQ ID NO: 118)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFFKYSMGWVRQAPGKGLEWVSIADTADRR  
 YYDHSVKGKRFITSRDNSKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFVYWGQGLT  
 VSS

>DOM1h-574-142 (SEQ ID NO: 119)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFFKYSMGWVRQAPGKGLEWVSIADTADRR  
 YYDHSVKGKRFITSRDNSKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFVYWGQGLT  
 VSS

>DOM1h-574-143 (SEQ ID NO: 120)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFFKYSMGWVRQAPGKGLEWVSIADTADRR  
 YYDDAVKGRFITSRDNSKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFVYWGQGLT  
 VSS

>DOM1h-574-144 (SEQ ID NO: 121)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFFKYSMGWVRQAPGKGLEWVSIADTADRR  
 YYDHSVKGKRFITSRDNSKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFVYWGQGLT  
 VSS

>DOM1h-574-145 (SEQ ID NO: 122)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFFKYSMGWVRQAPGKGLEWVSIADTADRR  
 YYDHSVKGKRFITSRDNSKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFVYWGQGLT  
 VSS

>DOM1h-574-146 (SEQ ID NO: 123)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFFKYSMGWVRQAPGKGLEWVSIADTADRR  
 YYDDAVKGRFITSRDNSKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFVYWGQGLT  
 VSS

>DOM1h-574-147 (SEQ ID NO: 124)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSIADTADRR  
 YYAHSVKGKRFITSRDNSKNTLYLQMNSLRAEDTAVYYCAIYTGRWGPVYWGQGLT  
 VSS

>DOM1h-574-148 (SEQ ID NO: 125)  
 EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSIADTADRR  
 YYAHSVKGKRFITSRDNSKNTLYLQMNSLRAEDTAVYYCAIYTGRWVFPYWGQGLT  
 VSS

TABLE 3-continued

Amino Acid Sequences of anti-TNFR1 dAbs
>DOM1h-574-149 (SEQ ID NO: 126) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTADRT  YYAHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWGPFQYWGQGLVT  VSS
>DOM1h-574-150 (SEQ ID NO: 127) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTADRT  YYAHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFQYWGQGLVT  VSS
>DOM1h-574-151 (SEQ ID NO: 128) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTADRT  YYAHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPPEYWGQGLVT  VSS
>DOM1h-574-152 (SEQ ID NO: 129) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTADRT  YYAHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPFQYWGQGLVT  VSS
>DOM1h-574-153 (SEQ ID NO: 130) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTADRT  YYAHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWVPPFQYWGQGLVT  VSS
>DOM1h-574-154 (SEQ ID NO: 131) EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQISDTGDRR  YYDHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPPEYWGQGLVT  VSS
>DOM1h-574-155 (SEQ ID NO: 132) EVQLLESGGGLVQPGGSLRRLSCAASGFTFLKYSMGWVRQAPGKGLEWVSQISDTADRT  YYAHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWVPPFQYWGQGLVT  VSS
>DOM1h-574-156 (SEQ ID NO: 133) EVQLLESGGGLVQPGGSLRRLSCAASGFTFFKYSMGWVRQAPGKGLEWVSQISDTADRT  YYAHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWVPPFQYWGQGLVT  VSS
>DOM1h-574-157 (SEQ ID NO: 134) EVQLLESGGGLVQPGGSLRRLSCAASGFTFLKYSMGWVRQAPGKGLEWVSQISDTADRT  YYDHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWRPPEYWGQGLVT  VSS
>DOM1h-574-158 (SEQ ID NO: 135) EVQLLESGGGLVQPGGSLRRLSCAASGFTFFKYSMGWVRQAPGKGLEWVSQISDTADRT  YYDHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWRPPEYWGQGLVT  VSS
>DOM1h-574-159 (SEQ ID NO: 136) EVQLLESGGGLVQPGGSLRRLSCAASGFTFFKYSMGWVRQAPGKGLEWVSQISDTADRT  YYDHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFVYWGQGLVT  VSS

TABLE 3-continued

## Amino Acid Sequences of anti-TNFR1 dAbs

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>DOM1h-574-160 (SEQ ID NO: 137)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFLKYSMGWVRQAPGKGLEWVSQISDTADRT  
YYDHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFVYWGQGLVT  
VSS

>DOM1h-574-161 (SEQ ID NO: 138)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFLKYSMGWVRQAPGKGLEWVSQISDTADRT  
YYSHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWVPPFEYWGQGLVT  
VSS

>DOM1h-574-162 (SEQ ID NO: 139)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFFKYSMGWVRQAPGKGLEWVSQISDTADRT  
YYSHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWVPPFEYWGQGLVT  
VSS

>DOM1h-574-163 (SEQ ID NO: 140)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFFKYSMGWVRQAPGKGLEWVSQISDTADRT  
YYTHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWVPPFEYWGQGLVT  
VSS

>DOM1h-574-164 (SEQ ID NO: 141)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFLKYSMGWVRQAPGKGLEWVSQISDTADRT  
YYTHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWVPPFEYWGQGLVT  
VSS

>DOM1h-574-165 (SEQ ID NO: 142)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFFKYSMGWVRQAPGKGLEWVSQISDTADRT  
YYAHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPFEYWGQGLVT  
VSS

>DOM1h-574-166 (SEQ ID NO: 143)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFLKYSMGWVRQAPGKGLEWVSQISDTADRT  
YYAHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPFEYWGQGLVT  
VSS

>DOM1h-574-167 (SEQ ID NO: 144)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFLKYSMGWVRQAPGKGLEWVSQISDTGDRR  
YYDHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPFEYWGQGLVT  
VSS

>DOM1h-574-169 (SEQ ID NO: 145)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQIADTADRT  
YYAHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWVPPFEYWGQGLVT  
VSS

>DOM1h-574-170 (SEQ ID NO: 146)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFFKYSMGWVRQAPGKGLEWVSQISDTADRT  
YYAHAVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWVPPFEYWGQGLVT  
VSS

>DOM1h-574-171 (SEQ ID NO: 147)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSQIADTADRT  
YYDHSVKGGRFTISRDN SKNTLYLQMNSLRAEDTAVYYCAIYTGRWVPPFEYWGQGLVT  
VSS

TABLE 3-continued

## Amino Acid Sequences of anti-TNFR1 dAbs

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>DOM1h-574-172 (SEQ ID NO: 148)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSIADTADR  
YYDHAVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAIYTGRWVPPFEYWGQGLVT  
VSS

>DOM1h-574-173 (SEQ ID NO: 149)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSIADTADR  
YYAHSVKGRTISRDNKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPFEYWGQGLVT  
VSS

>DOM1h-574-174 (SEQ ID NO: 150)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSIADTADR  
YYAHAVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPFEYWGQGLVT  
VSS

>DOM1h-574-175 (SEQ ID NO: 151)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSIADTADR  
YYAHAVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPFEYWGQGLVT  
VSS

>DOM1h-574-176 (SEQ ID NO: 152)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSIADTADR  
YYDHAVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPFEYWGQGLVT  
VSS

>DOM1h-574-177 (SEQ ID NO: 153)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSIADTADR  
YYDHAVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPFEYWGQGLVT  
VSS

>DOM1h-574-178 (SEQ ID NO: 154)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSIADTADR  
YYDHSVKGRTISRDNKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPFEYWGQGLVT  
VSS

>DOM1h-574-179 (SEQ ID NO: 155)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSIADTADR  
YYDDAVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAIYTGRWEPFVYWGQGLVT  
VSS

>DOM1h-574-180 (SEQ ID NO: 156)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSIADTADR  
YYAHAVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAIYTGRWVPPFEYWGQGLVT  
VSS

>DOM1h-574-4 (SEQ ID NO: 157)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSIADTADR  
YYADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKYTGRWEPFEYWGQGLVT  
VSS

>DOM1h-574-168 (SEQ ID NO: 158)  
EVQLLESGGGLVQPGGSLRRLSCAASGFTFVKYSMGWVRQAPGKGLEWVSIADTADR  
YYDHSVKGRTISRDNKNTLYLQMNSLRAEDTAVYYCAIYTGRWAPFEYWGQGLVT  
VSS

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TABLE 4

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-509 (SEQ ID NO: 157)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTAGTCAGTATAGGATGCATTGGGTCCGCCA  
 GGCTCCAGGGAAGAGTCTAGAGTGGGTCTCAAGTATTGATACTAGGGTTCGTCTACA  
 TACTACGCAGACCCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GAAAGCTGTGACGATGTTTTCTCCTTTTTTTGACTACTGGGGTCAGGGAACCTGGTC  
 ACCGTCTCGAGC

>DOM1h-510 (SEQ ID NO: 158)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGCTGATTATGGGATGCATTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTACGCGGACTGGTTCGTGTTACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GAAATGGCGGAATCGGCATGGTGAGTATCTTGTGATTTTGACTACTGGGGTCAGGGA  
 ACCCTGGTCACCGTCTCGAGC

>DOM1h-543 (SEQ ID NO: 159)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTATGAGGTATAGGATGCATTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCGATTGATTCTAATGGTTCAGTACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GAAAGATCGTACGGAGCGTTCGCCGGTTTTTGGACTACTGGGGTCAGGGAACCTGGTC  
 ACCGTCTCGAGC

>DOM1h-549 (SEQ ID NO: 160)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTGCAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTGATTATGAGATGCATTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCATCTATTAGTGAAGTGGTACGACGACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GAAACGTCGTTTTTCTGCTTCTACGTTTGGACTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574 (SEQ ID NO: 161)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTGAAATACGGGTGGTCATAACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GAAATATACGGGTCATTGGGAGCCTTTTGGACTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-1 (SEQ ID NO: 162)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTCACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCGAATACGGGTGGTCATAACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GAAATATACGGGTCGTTGGGAGCCTTATGACTACTGGGGTCAGGGAACCCCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-2 (SEQ ID NO: 163)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTCACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCGAATACGGGTGGTCATAACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GAAATATACGGGTCGTTGGGAGCCTTTTACTACTGGGGTCAGGGAACCCCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-4 (SEQ ID NO: 164)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTCACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCGAATACGGGTGGTCATAACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GAAATATACGGGTCGTTGGGAGCCTTTTACTACTGGGGTCAGGGAACCCCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-180 (SEQ ID NO: 165)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTCACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTGGATACTGCTGATCGTACA  
 TACTACGCACACCGGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
 GATATATACTGGGCGTTGGGTGCCTTTTACTACTGGGGTCAGGGAACCCCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-7 (SEQ ID NO: 166)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTCACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCGAATACGGGTGGTCATAACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTACTACTGGGGTCAGGGAACCCCTGGTCACC  
 GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-8 (SEQ ID NO: 167)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTCACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGTCCTAGAGTGGGTCTCACAGATTTCAATACGGGTGGTCATAACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCCCTGGTCACA  
 GTCTCGAGC

>DOM1h-574-9 (SEQ ID NO: 168)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTCACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGTCCTAGAGTGGGTCTCACAGATTTCAATACGGGTGGTCATAACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATATCCCGCGACAATCCAAGAACA  
 CGCTGTATATGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCCCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-10 (SEQ ID NO: 169)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTCACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGATCTAGAGTGGGTCTCACAGATTTCAATACGGGTGGTCATAACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCCCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-11 (SEQ ID NO: 170)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTCACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGTCCTAGAGTGGGTCTCACAGATTTCAATACGGGTGGTCATAACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GAAATATACGGGTCGTTGGGAGCCTTTTGACCCTGGGGTCAGGGGACCCCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-12 (SEQ ID NO: 171)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTCACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGTCCTAGAGTGGGTCTCACAGATTTCAATACGGGTGGTCATAACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GAAATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCCCTGGTCACC  
 GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-13 (SEQ ID NO: 172)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GAAATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-14 (SEQ ID NO: 173)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-15 (SEQ ID NO: 174)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCATAACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-16 (SEQ ID NO: 175)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGATGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCCAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCTGGTCACA  
 GTCTCGAGC

>DOM1h-574-17 (SEQ ID NO: 176)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGATGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCCAGAGTGGGTCTCACAGATTTCAATACGGGTGATCATAACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCTGGTCACA  
 GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-18 (SEQ ID NO: 177)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGGTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGATCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-19 (SEQ ID NO: 178)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGGTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGATCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCATA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-25 (SEQ ID NO: 179)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGGTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGATCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-26 (SEQ ID NO: 180)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGGTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGATCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-27 (SEQ ID NO: 181)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGGTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGATCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-28 (SEQ ID NO: 182)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTCACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTACA  
TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
GATATATACTGGCGTTGGGTGCCTTTTGTAGTACTGGGGTCAAGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-29 (SEQ ID NO: 183)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTCACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTACA  
TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGAGGCCTTTTGTAGTACTGGGGTCAAGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-30 (SEQ ID NO: 184)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTCACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTGCAATACGGGTGATCGTAGA  
TACTACGCAGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGAGCCTTTTGTACTACTGGGGTCAAGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-31 (SEQ ID NO: 185)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTCACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTACA  
TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGAGCCTTTTAACTACTGGGGTCAAGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-32 (SEQ ID NO: 186)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTCACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTACA  
TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGAGCCTTTTGTAGTACTGGGGTCAAGGAACCTGGTCACC  
GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-33 (SEQ ID NO: 187)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACT  
 CGCTGTATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGTGCCTTTTGACAACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-35 (SEQ ID NO: 188)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTATTACGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTTCAGTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-36 (SEQ ID NO: 189)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGGTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTACA  
 TACTACGGGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-37 (SEQ ID NO: 190)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTTTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTACA  
 TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAATGAACAGCCTGCGTGCCGAAGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-38 (SEQ ID NO: 191)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTAGA  
 TACTACGATGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

TABLE 4-continued

Nucleotide sequences of anti-TNFR1 dAbs
>DOM1h-574-39 (SEQ ID NO: 192) GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTAGA TACTACGCAGACGCGGTGAAGGGCGGTTACCATCTCCCGCGACAATCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCTGGTCACC GTCTCGAGC
>DOM1h-574-40 (SEQ ID NO: 193) GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTAGA TACTACGCAGACTCCGTGAAGGGCGGTTACCATCTCCCGCGACAATCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC GATATATACGGGTCGTTGGGAGCCTTTTAAGTACTGGGGTCAGGGAACCTGGTCACC GTCTCGAGC
>DOM1h-574-53 (SEQ ID NO: 194) GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  TCTCCTGTGCAGCCTCCGGATTACCTTTAGTAAGTATTCGATGGGGTGGGTCCGCCA GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGAGCGTAGA TACTACGCAGACTCAGTGAAGGGCGGTTACCATCTCCCGCGACAATCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC GATATATACGGGTCGGTGGGAGCCTTTTGAATACTGGGGTCAGGGAACCTGGTCACC GTCTCGAGC
>DOM1h-574-54 (SEQ ID NO: 195) GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTAGA TACTACGCGACTCCGTGAAGGGCGGTTACCATCTCCCGCGACAATCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC GATATATACGGGTCGTTGGGAGCCTTATGAGTACTGGGGTCAGGGAACCTGGTCACC GTCACGAGC
>DOM1h-574-65 (SEQ ID NO: 196) GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTAGA TACTACGCAGACTCTGTGAAGGGCGGTTACCATCTCCCGGATAATCCAAGAACA CACTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC GATATATACGGGTCGTTGGGAGCCTTTTGTCTACTGGGGTCAGGGAACCTGGTCACC GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-66 (SEQ ID NO: 197)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTGCGAATACGGGTGATCGTAGA  
 TACTACGCAGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGAAGCCTTTTGTAGTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-67 (SEQ ID NO: 198)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTGCGAATACGGGTGATCGTAGA  
 TACTACGCAGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
 GATATATACTGGGCGTTGGGTGCCTTTTGTAGTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-68 (SEQ ID NO: 199)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTGCGAATACGGGTGATCGTAGA  
 TACTACGCAGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGAGGCTTTTGTAGTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-69 (SEQ ID NO: 200)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTGCGAATACGGGTGATCGTAGA  
 TACTACGCAGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGCGCCTTTTGTAGTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-70 (SEQ ID NO: 201)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTGCGAATACTGCTGATCGTACA  
 TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GGTATATACGGGTCGTTGGGAGCCTTTTGTCTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-71 (SEQ ID NO: 202)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACTGCTGATCGTACA  
 TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGAAGCCTTTTGTAGTACTGGGGTCAGGGAACCCCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-72 (SEQ ID NO: 203)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACTGCTGATCGTACA  
 TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
 GATATATACTGGGCTTGGGTGCCTTTTGTAGTACTGGGGTCAGGGAACCCCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-73 (SEQ ID NO: 204)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACTGCTGATCGTACA  
 TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGAGGCTTTTGTAGTACTGGGGTCAGGGAACCCCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-74 (SEQ ID NO: 205)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACTGCTGATCGTACA  
 TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGCGCCTTTTGTAGTACTGGGGTCAGGGAACCCCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-75 (SEQ ID NO: 206)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACTGCTGATCGTAGA  
 TACTACGATGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGTCTACTGGGGTCAGGGAACCCCTGGTCACC  
 GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-76 (SEQ ID NO: 207)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCCCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACGGGTGATCGTAGA  
TACTACGATGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGAAGCCTTTTGTAGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-77 (SEQ ID NO: 208)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACGGGTGATCGTAGA  
TACTACGATGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACTGGGCGTTGGGTGCCTTTTGTAGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-78 (SEQ ID NO: 209)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACGGGTGATCGTAGA  
TACTACGATGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGAGGCTTTTGTAGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-79 (SEQ ID NO: 210)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACGGGTGATCGTAGA  
TACTACGATGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGAGGCTTTTGTAGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-84 (SEQ ID NO: 211)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACGGGTGATCGTAGA  
TACTACGATGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGAGGCTTTTGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-85 (SEQ ID NO: 212)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTAGA  
TACTACGCAGACGCGGTGAAGGGCGGTTACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGAAGCCTTTTGGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-86 (SEQ ID NO: 213)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCCCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTAGA  
TACTACGCAGACGCGGTGAAGGGCGGTTACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGACACCGCGGTATATTACTGTGC  
GATATATACTGGGCTGTTGGGTGCCTTTTGGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-87 (SEQ ID NO: 214)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTAGA  
TACTACGCAGACGCGGTGAAGGGCGGTTACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGAGGCTTTTGGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-88 (SEQ ID NO: 215)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTAGA  
TACTACGCAGACGCGGTGAAGGGCGGTTACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGAGGCTTTTGGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-90 (SEQ ID NO: 216)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTGAAGTTTTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACGGGTGATCGTAGA  
TACTACGCAGACTCTGTGAAGGGCGGTTACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGCGCCTTTTGGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-91 (SEQ ID NO: 217)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTGAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTGGAATACTGCTGATCGTACA  
TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGGTGGGCGCCTTTTGTACTGAGTACTGGGGTACAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-92 (SEQ ID NO: 218)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTCAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTGGATACGGGTGATCGTAGA  
TACTACGATGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGGTGGGAGCCTTTTGTCTACTGAGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-93 (SEQ ID NO: 219)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTGAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTGGATACGGGTGATCGTAGA  
TACTACGATGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGGTGGGAGCCTTTTGTCTACTGAGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-94 (SEQ ID NO: 220)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTAAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTGGAATACTGCTGATCGTACA  
TACTACGCAGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGCATATTACTGTGC  
GATATATACGGGTCGGTGGCCGACTTTGACTACTGAGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-95 (SEQ ID NO: 221)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTAAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTGGAATACTGCTGATCGTACA  
TACTACGCAGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGCATATTACTGTGC  
GATATATACGGGTCGGTGGCCGACTTTGACTACTGAGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

TABLE 4-continued

Nucleotide sequences of anti-TNFR1 dAbs
>DOM1h-574-96 (SEQ ID NO: 222) GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACTGCTGATCGTACA TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC GATATATACGGGTCGGTGGCCCGACTTTGACTACTGGGGTCAGGGAACCTGGTCACC GTCTCGAGC
>DOM1h-574-97 (SEQ ID NO: 223) GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCAATACTGCTGATCGTACA TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC GATATATACGGGTCGGTGGCCCGACTTTGACTACTGGGGTCAGGGAACCTGGTCACC GTCTCGAGC
>DOM1h-574-98 (SEQ ID NO: 224) GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTGCGATACGGGTGATCGTAGA TACTACGATGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC GATATATACGGGTCGGTGGCCCGACTTTGACTACTGGGGTCAGGGAACCTGGTCACC GTCTCGAGC
>DOM1h-574-99 (SEQ ID NO: 225) GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTGCGATACGGGTGATCGTAGA TACTACGATGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC GATATATACGGGTCGGTGGCCCGACTTTGACTACTGGGGTCAGGGAACCTGGTCACC GTCTCGAGC
>DOM1h-574-100 (SEQ ID NO: 226) GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGATGGGTCCGCCA GGCTCCAGGGAAGGGTCCAGAGTGGGTCTCACAGATTTGCGCTGGGGTGACAGGACA TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC GATATATACGGGTCGGTGGGAGCCTTTGACTACTGGGGTCAGGGAACCTGGTCACC GTCTCGAGC

TABLE 4-continued

Nucleotide sequences of anti-TNFR1 dAbs
>DOM1h-574-101 (SEQ ID NO: 227) GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA GGCTCCAGGGAAGGTCCAGAGTGGGTCTCACAGATTTCCGACGGCGGTCCAGAGGACA TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCTGGTCACC GTCTCGAGC
>DOM1h-574-102 (SEQ ID NO: 228) GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGATGGGTCCGCCA GGCTCCAGGGAAGGTCCAGAGTGGGTCTCACAGATTTCCGACTCCGGTTACCGCACA TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCTGGTCACC GTCTCGAGC
>DOM1h-574-103 (SEQ ID NO: 229) GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA GGCTCCAGGGAAGGTCCAGAGTGGGTCTCACAGATTTCCGACGGGGTACGCGGACA TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCTGGTCACC GTCTCGAGC
>DOM1h-574-104 (SEQ ID NO: 230) GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGATGGGTCCGCCA GGCTCCAGGGAAGGTCCAGAGTGGGTCTCACAGATTTCCGACAAGGGTACGCGCACA TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCTGGTCACC GTCTCGAGC
>DOM1h-574-105 (SEQ ID NO: 231) GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGATGGGTCCGCCA GGCTCCAGGGAAGGTCCAGAGTGGGTCTCACAGATTTCCGAGACCGGTCCGAGGACA TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCTGGTCACC GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-106 (SEQ ID NO: 232)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTAACAATACGGGTTCGACCACA  
TACTACGCAGACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGAGCCTTTTGACTACTGGGGTCAGGGAACCCCTGGTCACC  
GTCTCGAGC

>DOM1h-574-107 (SEQ ID NO: 233)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCCAGAGTGGGTCTCACAGATTTGAATACTGCTGATCGTACA  
TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
GATATATACTGGGCGTTGGGTGCCTTTTGAGTACTGGGGTCAGGGAACCCCTGGTCACC  
GTCTCGAGC

>DOM1h-574-108 (SEQ ID NO: 234)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCCAGAGTGGGTCTCACAGATTTGAATACTGCTGATCGTACA  
TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGGTGGGCGCCTTTTGAGTACTGGGGTCAGGGAACCCCTGGTCACC  
GTCTCGAGC

>DOM1h-574-109 (SEQ ID NO: 235)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTGGATACTGCTGATCGTACA  
TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
GATATATACTGGGCGTTGGGTGCCTTTTGAGTACTGGGGTCAGGGAACCCCTGGTCACC  
GTCTCGAGC

>DOM1h-574-110 (SEQ ID NO: 236)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTGGATACTGCTGATCGTACA  
TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGGTGGGCGCCTTTTGAGTACTGGGGTCAGGGAACCCCTGGTCACC  
GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-111 (SEQ ID NO: 237)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
 TACTACGATGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGGTGGGCGCCTTTTGGAGTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-112 (SEQ ID NO: 238)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
 TACTACACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGGTGGGCGCCTTTTGGAGTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-113 (SEQ ID NO: 239)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTGAACTACTGCTGATCGCAGA  
 TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGGTGGGCGCCTTTTGGAGTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-114 (SEQ ID NO: 240)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTGAACTACTGCTGATCGTACA  
 TACTACGATCACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGGTGGGCGCCTTTTGGAGTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-115 (SEQ ID NO: 241)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTGAACTACTGCTGATCGTACA  
 TACTACGATCACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGGTGGGCGCCTTTTGGAGTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-116 (SEQ ID NO: 242)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTAGA  
 TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATAACGGGTCGGTGGGCGCCTTTTGTAGTACTGGGGTACAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-117 (SEQ ID NO: 243)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTAGA  
 TACTACGATCACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATAACGGGTCGGTGGGCGCCTTTTGTAGTACTGGGGTACAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-118 (SEQ ID NO: 244)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTGAAATACTGCTGATCGTACA  
 TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GGATATACTGGGCGTTGGGTGTCTTTTGTAGTACTGGGGTACAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-119 (SEQ ID NO: 245)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTGAAATACTGCTGATCGTACA  
 TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GCTATATACTGGGCGTTGGGTGTCTTTTGTAGTACTGGGGTACAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-120 (SEQ ID NO: 246)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTGAAATACTGCTGATCGTACA  
 TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GGTATATACTGGGCGTTGGGTGTCTTTTGTAGTACTGGGGTACAGGGAACCTGGTCACC  
 GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-121 (SEQ ID NO: 247)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTCGAATACTGCTGATCGTACA  
TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GCTATATACTGGCGTTGGGTGCCTTTTGTAGTACTGGGGTACAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-122 (SEQ ID NO: 248)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTCGAATACTGCTGATCGTAGA  
TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGCGCCTTTTGTAGTACTGGGGTACAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-123 (SEQ ID NO: 249)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTCGAATACTGCTGATCGTAGA  
TACTACGCAGACGCGGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGAGCCTTTTGTCTACTGGGGTACAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-124 (SEQ ID NO: 250)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCGGCCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTCGAATACGGGCGATCGTAGA  
TACTACGCACACGCGGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGAGCCTTTTGTCTACTGGGGTACAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-125 (SEQ ID NO: 251)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTCGAATACTGCTGATCGTAGA  
TACTACGCAGACGCGGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGAGCCTTTTGTCTACTGGGGTACAGGGAACCTGGTCACC  
GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-126 (SEQ ID NO: 252)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTGCGAATACGGGTGATCGTAGA  
 TACTACGCACACGCGGTGAAGGGGCGTTACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGTCTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-127 (SEQ ID NO: 253)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTCGAATACTGCTGATCGTAGA  
 TACTACGCACACGCGGTGAAGGGGCGTTACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGTCTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-128 (SEQ ID NO: 254)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTGCGAATACGGGTGATCGTAGA  
 TACTACGCACACGCGGTGAAGGGGCGTTACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGTCTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-129 (SEQ ID NO: 255)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTGTAATACGGGTGATCGTAGA  
 TACTACGCAGACGCGGTGAAGGGGCGTTACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGTCTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-130 (SEQ ID NO: 256)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTGCGAATACGGGTGATCGTAGA  
 TACTACGCAGACGCGGTGAAGGGGCGTTACCATCTCCCGCGACAATCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGAGCCTTTTGTCTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-131 (SEQ ID NO: 257)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACGATCACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGCGCCTTTTGTAGTACTGGGGTACAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-132 (SEQ ID NO: 258)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACGATCACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGAGGCCCTTTTGTAGTACTGGGGTACAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-133 (SEQ ID NO: 259)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACGATCACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGAGCCCTTTTGTCTACTGGGGTACAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-134 (SEQ ID NO: 260)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACTCACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
GATATATACTGGGCGTTGGGTGCCTTTTGTAGTACTGGGGTACAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-135 (SEQ ID NO: 261)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
GATATATACTGGGCGTTGGGTGCCTTTTGTAGTACTGGGGTACAGGGAACCTGGTCACC  
GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-137 (SEQ ID NO: 262)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
 TACTACACAGACGCGGTGAAGGGCGGTTACCATCTCCCGCACAATTCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGGTGGGAGCCTTTTGTCTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-138 (SEQ ID NO: 263)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTTTCAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
 TACTACGCACACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGGTGGGCGCCTTTTGTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-139 (SEQ ID NO: 264)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTTTGAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
 TACTACGCACACTCCGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGGTGGGCGCCTTTTGTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-140 (SEQ ID NO: 265)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTTTCAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTAGA  
 TACTACGATGACTCTGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGGTGGGAGCCTTTTGTCTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-141 (SEQ ID NO: 266)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTTTCAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTAGA  
 TACTACGATGACTCTGTGAAGGGCCGGTTACCATCTCCCGCACAATTCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGGTGGGAGCCTTTTGTCTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-142 (SEQ ID NO: 267)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTCAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTCGGATACGGGTGATCGTAGA  
TACTACGATCACTCTGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGAACCTTTTGTCTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-143 (SEQ ID NO: 268)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTCAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTCGGATACGGGTGATCGTAGA  
TACTACGATGACGCGGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGAGCCTTTTGTCTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-144 (SEQ ID NO: 269)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTCAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTGCGGATACTGCTGATCGTAGA  
TACTACGATGACTCTGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGAGCCTTTTGTCTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-145 (SEQ ID NO: 270)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTCAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTGCGGATACTGCTGATCGTAGA  
TACTACGATCACTCTGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGAGCCTTTTGTCTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-146 (SEQ ID NO: 271)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTCAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTGCGGATACTGCTGATCGTAGA  
TACTACGATGACGCGGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGAGCCTTTTGTCTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-147 (SEQ ID NO: 272)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGGCCCTTTTGTCTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-148 (SEQ ID NO: 273)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGTGCCCTTTTGCCTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-149 (SEQ ID NO: 274)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGGACCTTTTTCAGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-150 (SEQ ID NO: 275)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGAGCCTTTTTCAGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-151 (SEQ ID NO: 276)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGCGCCTTTTGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-152 (SEQ ID NO: 277)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
 TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGCGCCTTTTCAGTACTGGGGTCAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-153 (SEQ ID NO: 278)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
 TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGTTGGGTCCTTTTCAGTACTGGGGTCAGGGACCCCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-154 (SEQ ID NO: 279)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACCGGTGATCGTAGA  
 TACTACGATCACTCTGTGAAGGGCCGGTTCACTATCTCCCGCACAATTCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGGTCGGTGGGCGCCTTTTGAGTACTGGGGTCAGGGAACCCCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-155 (SEQ ID NO: 280)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTTGAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
 TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
 GATATATACTGGGCGTTGGGTGCCTTTTGAGTACTGGGGTCAGGGAACCCCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-156 (SEQ ID NO: 281)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTTCAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
 TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
 GATATATACTGGGCGTTGGGTGCCTTTTGAGTACTGGGGTCAGGGAACCCCTGGTCACC  
 GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-157 (SEQ ID NO: 282)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTGAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACGATCACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGAGGCCTTTTGAGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-158 (SEQ ID NO: 283)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTCAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACGATCACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGAGGCCTTTTGAGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-159 (SEQ ID NO: 284)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTCAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACGATCACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGAGCCTTTTGTCTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-160 (SEQ ID NO: 285)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTGAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACGATCACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGTTGGGAGCCTTTTGTCTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-161 (SEQ ID NO: 286)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTGAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACTCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
GATATATACTGGGCGTTGGGTGCCTTTTGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-162 (SEQ ID NO: 287)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTCAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACTCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
GATATATACTGGGCGTTGGGTGCCTTTTGAGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-163 (SEQ ID NO: 288)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTCAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
GATATATACTGGGCGTTGGGTGCCTTTTGAGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-164 (SEQ ID NO: 289)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTGAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
GATATATACTGGGCGTTGGGTGCCTTTTGAGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-165 (SEQ ID NO: 290)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTCAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGTTCGTTGGGCGCCTTTTGAGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-166 (SEQ ID NO: 291)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTGAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGTTCGTTGGGCGCCTTTTGAGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-167 (SEQ ID NO: 292)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTGAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACCGGTGATCGTAGA  
TACTACGATCACTCTGTGAAGGGCCGGTTCACTATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGGTGGGCGCCTTTTGTAGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-168 (SEQ ID NO: 293)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTCAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACCGGTGATCGTAGA  
TACTACGATCACTCTGTGAAGGGCCGGTTCACTATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGGTGGGCGCCTTTTGTAGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-169 (SEQ ID NO: 294)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTGCGATACTGCTGATCGTACA  
TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGCGC  
GATATATACTGGGCGTTGGGTGCCTTTTGTAGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-170 (SEQ ID NO: 295)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACGCACACCGGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
GATATATACTGGGCGTTGGGTGCCTTTTGTAGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

>DOM1h-574-171 (SEQ ID NO: 296)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTGCAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTCCGATACTGCTGATCGTACA  
TACTACGATCACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
GATATATACTGGGCGTTGGGTGCCTTTTGTAGTACTGGGGTCAGGGAACCTGGTCACC  
GTCTCGAGC

TABLE 4-continued

## Nucleotide sequences of anti-TNFR1 dAbs

>DOM1h-574-172 (SEQ ID NO: 297)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTGCGGATACTGCTGATCGTACA  
 TACTACGATCACGCGGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCTGAGGACACCGCGGTATATTACTGTGC  
 GATATATACTGGCGTTGGGTGCCTTTTGGTACTGGGGTACAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-173 (SEQ ID NO: 298)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTGCGGATACTGCTGATCGTAGA  
 TACTACGCACACTCCGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGTCCGTGGGCGCCTTTTGGTACTGGGGTACAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-174 (SEQ ID NO: 299)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTCGGATACTGCTGATCGTAGA  
 TACTACGCACACGCGGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGTCCGTGGGCGCCTTTTGGTACTGGGGTACAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-175 (SEQ ID NO: 300)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTCGGATACTGCTGATCGTAGA  
 TACTACGCACACGCGGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGTCCGTGGGCGCCTTTTGGTACTGGGGTACAGGGAACCTGGTCACC  
 GTCTCGAGC

>DOM1h-574-176 (SEQ ID NO: 301)  
 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
 TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
 GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTCGGATACTGCTGATCGTAGA  
 TACTACGATCACGCGGTGAAGGGCCGGTTCACCATCTCCCGCACAATTCCAAGAACA  
 CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
 GATATATACGGTCCGTGGGCGCCTTTTGGTACTGGGGTACAGGGAACCTGGTCACC  
 GTCTCGAGC

TABLE 4-continued

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Nucleotide sequences of anti-TNFR1 dAbs

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>DOM1h-574-177 (SEQ ID NO: 302)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTGCGGATACTGCTGATCGTAGA  
TACTACGATCACGCGGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGGTGGGCGCCTTTTGTAGTACTGGGGTCAGGGGACCCTGGTCACC  
GTCTCGAGC

>DOM1h-574-178 (SEQ ID NO: 303)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTGTTAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTGCGGATACTGCTGATCGTAGA  
TACTACGATCACTCCGTGAAGGGCCGGTTCACCATCTCCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGGTGGGCGCCTTTTGTAGTACTGGGGTCAGGGGACCCTGGTCACC  
GTCTCGAGC

>DOM1h-574-179 (SEQ ID NO: 304)  
GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGCGTC  
TCTCCTGTGCAGCCTCCGGATTACCTTTTCAAGTATTCGATGGGGTGGGTCCGCCA  
GGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACAGATTTGCGATACTGCTGATCGTAGA  
TACTACGATGACGCGGTGAAGGGCCGGTTCACCATCACCCGCGACAATCCAAGAACA  
CGCTGTATCTGCAAATGAACAGCCTGCGTGCCGAGGACACCGCGGTATATTACTGTGC  
GATATATACGGGTCGGTGGGAGCCTTTTGTCTACTGGGGTCAGGGGACCCTGGTCACC  
GTCTCGAGC

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TABLE 5

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Anti-serum albumin dAb (DOM7h) fusions

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(used in Rat studies):-  
DOM7h-14/Exendin-4 fusion DMS number 7138  
Amino acid sequence (SEQ ID NO: 305)  
HGEFTFTSDLKQMEEEAVRLFIEWLKNGGPSSGAPPPSGGGGSGGGGSGGG

GSDIQMTQSPSSLSASVGDRTVITCRASQWIGSQLSWYQQKPGKAPKLLIMWRS  
SLQSGVPSRFRFGSGSGTDFTLTISSLQPEDFATYYCAQGAALPRTFGQGTKVEIKR

Nucleotide sequence (SEQ ID NO: 306)  
CATGGTGAAGGAACATTTACCAGTGACTTGTCAAACAGATGGAAGAGGAG  
GCAGTGCGGTTATTTATTGAGTGGCTTAAGAACGAGGACCAAGTAGCGGG  
GCACCTCCGCCATCGGGTGGTGGAGGCGGTTTCAGGCGGAGGTGGCAGCGGC  
GGTGGCGGGTCGGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCAT  
CTGTAGGAGACCGTGTACCATCACTTGCCGGCAAGTCAGTGGATTGGGT  
CTCAGTTATCTTGGTACCAGCAGAAACCAGGAAAGCCCCTAAGCTCCTGA  
TCATGTGGCGTTCTCGTTGCAAAGTGGGGTCCCATCAGTTCAGTGGCAG  
TGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT

TABLE 5-continued

## Anti-serum albumin dAb (DOM7h) fusions

TTTGCTACGTACTACTGTGCTCAGGGTGCGGCGTTGCCTAGGACGTTCCGGCC

AAGGGACCAAGGTGGAATCAAACGG

DOM7h-14-10/Exendin-4 fusion DMS number 7139

Amino acid sequence (SEQ ID NO: 307)

HGEGTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPSGGGGSGGGGSGGG

GSDIQMTQSPSSLSASVGDRTITCRASQWIGSLSWYQQKPKKAPKLLIMWRS

SLQSGVPSRFRSGSGSGTDFTLTISSLQPEDFATYYCAQGLRHPKTFGQGTKVEIKR

Nucleotide sequence (SEQ ID NO: 308)

CATGGTGAAGGAACATTTACCAGTGACTTGTCAAACAGATGGAAGAGGAG

GCAGTGCGGTTATTTATTGAGTGGCTTAAGAACGGAGGACCAAGTAGCGGG

GCACCTCCGCCATCGGGTGGTGGAGGCGGTTTCAGGCGGAGGTGGCAGCGGC

GGTGGCGGGTCGGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCAT

CTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTCAGTGGATTGGGT

CTCAGTTATCTTGGTACCAGCAGAAACCAGGAAAGCCCTAAGCTCCTGA

TCATGTGGCGTTCCTCGTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAG

TGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT

TTTGCTACGTACTACTGTGCTCAGGGTTTGGAGCATCCTAAGACGTTCCGGCC

AAGGGACCAAGGTGGAATCAAACGG

DOM7h-14-18/Exendin-4 fusion DMS number 7140

Amino acid sequence (SEQ ID NO: 309)

HGEGTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPSGGGGSGGGGSGGG

GSDIQMTQSPSSLSASVGDRTITCRASQWIGSLSWYQQKPKKAPKLLIMWRS

SLQSGVPSRFRSGSGSGTDFTLTISSLQPEDFATYYCAQGLMKPMTFGQGTKVEIKR

Nucleotide sequence (SEQ ID NO: 310)

CATGGTGAAGGAACATTTACCAGTGACTTGTCAAACAGATGGAAGAGGAG

GCAGTGCGGTTATTTATTGAGTGGCTTAAGAACGGAGGACCAAGTAGCGGG

GCACCTCCGCCATCGGGTGGTGGAGGCGGTTTCAGGCGGAGGTGGCAGCGGC

GGTGGCGGGTCGGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCAT

CTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTCAGTGGATTGGGT

CTCAGTTATCTTGGTACCAGCAGAAACCAGGAAAGCCCTAAGCTCCTGA

TCATGTGGCGTTCCTCGTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAG

TGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT

TTTGCTACGTACTACTGTGCTCAGGGTCTTATGAAGCCTATGACGTTCCGGCC

AAGGGACCAAGGTGGAATCAAACGG

DOM7h-14-19/Exendin-4 fusion DMS number 7141

Amino acid sequence (SEQ ID NO: 311)

HGEGTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPSGGGGSGGGGSGGG

GSDIQMTQSPSSLSASVGDRTITCRASQWIGSLSWYQQKPGKAPKLLIMWRS

SLQSGVPSRFRSGSGSGTDFTLTISSLQPEDFATYYCAQGAALPRTFGQGTKVEIKR

Nucleotide sequence (SEQ ID NO: 312)

CATGGTGAAGGAACATTTACCAGTGACTTGTCAAACAGATGGAAGAGGAG

GCAGTGCGGTTATTTATTGAGTGGCTTAAGAACGGAGGACCAAGTAGCGGG

GCACCTCCGCCATCGGGTGGTGGAGGCGGTTTCAGGCGGAGGTGGCAGCGGC

GGTGGCGGGTCGGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCAT

TABLE 5-continued

Anti-serum albumin dAb (DOM7h) fusions

CTGTAGGAGACCGTGTACCATCTCTTGCCGGCAAGTCAGTGGATTGGGTC  
 TCAGTTATCTTGGTACCAGCAGAAAACCAGGGGAAGCCCTAAGCTCCTGAT  
 CATGTGGCGTTCTCGTTGCAAAGTGGGGTCCCATCAGTTTTCAGTGGCAGT  
 GGATCTGGGACAGATTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATT  
 TTGCTACGTACTACTGTGCTCAGGGTGC GGCGTTGCCTAGGACGTTCCGGCCA  
 AGGGACCAAGGTGAAATCAAACGG  
 DOM7h-11/Exendin-4 fusion DMS number 7142  
 Amino acid sequence (SEQ ID NO: 313)  
 HGEFTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPSGGGGSGGGGSGGG  
 GSDIQMTQSPSSLSASVGDVRTITCRASRPITGLSWYQQKPGKAPKLLIWFGR  
 LQSGVPSRFRSGSGTDFTLTISLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR  
 Nucleotide sequence (SEQ ID NO: 314)  
 CATGGTGAAGGAACATTTACCAGTACTTGTCAAACAGATGGAAGAGGAG  
 GCAGTGC GGTTATTTATTGAGTGGCTTAAGAACGGAGGACCAAGTAGCGGG  
 GCACCTCCGCCATCGGGTGGTGGAGGCGGTTACAGCGGAGGTGGCAGCGGC  
 GGTGGCGGGTCCGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCAT  
 CTGTAGGAGACCGTGTACCATCACTTGCCGGCAAGTCGTCGGATTGGGA  
 CGACGTTAAGTTGGTACCAGCAGAAAACCAGGAAAGCCCTAAGCTCCTGA  
 TCTGGTTTGGTTCCCGTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAG  
 TGGATCTGGGACAGATTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT  
 TTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACGACGTTCCGGCC  
 AAGGGACCAAGGTGAAATCAAACGG  
 DOM7h-11-12/Exendin-4 fusion DMS number 7147  
 Amino acid sequence (SEQ ID NO: 315)  
 HGEFTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPSGGGGSGGGGSGGG  
 GSDIQMTQSPSSLSASVGDVRTITCRASRPITGLSWYQQKPGKAPKLLILFGR  
 LQSGVPSRFRSGSGTDFTLTISLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR  
 Nucleotide sequence (SEQ ID NO: 316)  
 CATGGTGAAGGAACATTTACCAGTACTTGTCAAACAGATGGAAGAGGAG  
 GCAGTGC GGTTATTTATTGAGTGGCTTAAGAACGGAGGACCAAGTAGCGGG  
 GCACCTCCGCCATCGGGTGGTGGAGGCGGTTACAGCGGAGGTGGCAGCGGC  
 GGTGGCGGGTCCGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCAT  
 CTGTAGGAGACCGTGTACCATCACTTGCCGGCAAGTCGTCGGATTGGGA  
 CGATGTTAAGTTGGTACCAGCAGAAAACCAGGAAAGCCCTAAGCTCCTGA  
 TCTTGGTTTGGTTCCCGTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAG  
 TGGATCTGGGACAGATTCACTCTCACCATCAGCAGTCTGCAACCTGAAGAT  
 TTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACGACGTTCCGGCC  
 AAGGGACCAAGGTGAAATCAAACGG  
 DOM7h-11-15/Exendin-4 fusion DMS number 7143  
 Amino acid sequence (SEQ ID NO: 317)  
 HGEFTFTSDLSKQMEEEAVRLFIEWLKNGGPSSGAPPPSGGGGSGGGGSGGG  
 GSDIQMTQSPSSLSASVGDVRTITCRASRPITGLSWYQQKPGKAPKLLILAFSR  
 LQSGVPSRFRSGSGTDFTLTISLQPEDFATYYCAQAGTHPTTFGQGTKVEIKR

TABLE 5-continued

Anti-serum albumin dAb (DOM7h) fusions

Nucleotide sequence (SEQ ID NO: 318)

CATGGTGAAGGAACATTTACCAGTGACTTGTCAAACAGATGGAAGAGGAG

GCAGTGCGGTTATTTATTGAGTGGCTTAAGAACGGAGGACCAAGTAGCGGG

GCACCTCCGCCATCGGGTGGTGGAGGCGGTTTCAGGCGGAGGTGGCAGCGGC

GGTGGCGGGTCGGACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCAT

CTGTAGGAGACCGTGTACCATCACTTGCCTGGCAAGTCGTCCGATTGGGA

CGATGTTAAGTTGGTACCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGA

TCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGT

GGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATT

TTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCA

AGGGACCAAGGTGAAATCAAACGG

DOM7h14-10/G4SC-NCE fusion

Amino acid sequence (SEQ ID NO: 319) encoding DOM7h14-10/G4SC

DIQMTQSPSSLSASVGDRTVITCRASQWIGSQLSWYQQKPKKAPKLLIMWRSSL

QSGVPSRPSGSGSGTDFTLTISLQPEDFATYYCAQGLRHPKTFGQTKVEIKRG

GGGSC

The C-terminal cysteine can be linked to a new chemical entity (pharmaceutical chemical compound, NCE), eg using maleimide linkage.

Nucleotide sequence (SEQ ID NO: 320) encoding DOM7h14-10/G4SC

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACC

GTGTACCATCACTTGCCTGGCAAGTCAGTGGATTGGGTCTCAGTTATCTTG

GTACCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCATGTGGCGTTC

CTCGTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGAC

AGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCTACGTAC

TACTGTGCTCAGGGTTTGAGGCATCCTAAGACGTTTCGGCCAAGGACCAAG

GTGAAATCAAACGGGGTGGCGGAGGGGGTTCCTGT

DOM7h14-10/TVAAPSC fusion

Amino acid sequence (SEQ ID NO: 321)

DIQMTQSPSSLSASVGDRTVITCRASQWIGSQLSWYQQKPKKAPKLLIMWRSSL

QSGVPSRPSGSGSGTDFTLTISLQPEDFATYYCAQGLRHPKTFGQTKVEIKRT

VAAPSC

The C-terminal cysteine can be linked to a new chemical entity (pharmaceutical chemical compound, NCE), eg using maleimide linkage.

Nucleotide sequence (SEQ ID NO: 322)

GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACC

GTGTACCATCACTTGCCTGGCAAGTCAGTGGATTGGGTCTCAGTTATCTTG

GTACCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCATGTGGCGTTC

CTCGTTGCAAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATCTGGGAC

AGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTGCTACGTAC

TACTGTGCTCAGGGTTTGAGGCATCCTAAGACGTTTCGGCCAAGGACCAAG

GTGAAATCAAACGGACCGTCTGCTCCATCTTGT

(used in mouse studies):-

DOM7h-11/DOM1m-21-23 fusion DMS number 5515

Amino acid sequence (SEQ ID NO: 323)

EVQLLESGGGLVQPGGSLRLSCAASGFTFNRYSMGWLRQAPGKGLEWVSRIDS

YGRGTYIEDPVKGRFSISRDNKNTLYLQMNSLR AEDTAVYYCAKISQFGSNA

TABLE 5-continued

Anti-serum albumin dAb (DOM7h) fusions

FDYWGQGTQVTVSSASTSGPSDIQMTQSPSSLSASVGDVRTITCRASRPIGTTLS

WYQQKPGKAPKLLIWFGSRLQSGVPSRFGSGSGTDFTLTISLQPEDFATYYC

AQAQTHPTTFGQGTKVEIKR

Amino acid plus nucleotide plus myc tag sequence (SEQ ID NO: 324)

EVQLLESGGGLVQPGGSLRLSCAASGFTFNRYSMGWLRQAPGKLEWVSRIDS

YGRGTYIEDPVKGRFSISRDNKNTLYLQMNSLRAEDTAVYYCAKISQFGSNA

FDYWGQGTQVTVSSASTSGPSDIQMTQSPSSLSASVGDVRTITCRASRPIGTTLS

WYQQKPGKAPKLLIWFGSRLQSGVPSRFGSGSGTDFTLTISLQPEDFATYYC

AQAQTHPTTFGQGTKVEIKRAAAEQKLISEEDLN

Nucleotide sequence (SEQ ID NO: 325)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCC

CTGCGTCTCTCCTGTGCAGCCTCCGGATTACCTTTAATAGGTATAGTATGG

GGTGGCTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGGATTG

ATTCTTATGGTCGTGGTACATACTACGAAGACCCCGTGAAGGGCCGGTTCA

GCATCTCCCGGACAATCCAAGAACACGCTGTATCTGCAAATGAACAGCC

TGCGTGCCGAGGACACCGCGTATATTACTGTGCGAAAATTTCTCAGTTTGG

GTCAAATGCGTTTGACTACTGGGGTCAGGGAACCCAGGTCACCGTCTCGAG

CGCTAGCACCAGTGGTCCATCGGACATCCAGATGACCCAGTCTCCATCCTCC

CTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTCGTC

CGATTGGGACGACGTTAAGTTGGTACCAGCAGAAACCAGGGAAGCCCTA

AGCTCCTGATCTGGTTTGGTCCCGGTTGCAAAGTGGGGTCCCATCACGTTT

CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCA

ACCTGAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACG

ACGTTCCGCCAAGGGACCAAGGTGGAAATCAAACGG

Nucleotide plus myc tag sequence (SEQ ID NO: 326)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCC

CTGCGTCTCTCCTGTGCAGCCTCCGGATTACCTTTAATAGGTATAGTATGG

GGTGGCTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGGATTG

ATTCTTATGGTCGTGGTACATACTACGAAGACCCCGTGAAGGGCCGGTTCA

GCATCTCCCGGACAATCCAAGAACACGCTGTATCTGCAAATGAACAGCC

TGCGTGCCGAGGACACCGCGTATATTACTGTGCGAAAATTTCTCAGTTTGG

GTCAAATGCGTTTGACTACTGGGGTCAGGGAACCCAGGTCACCGTCTCGAG

CGCTAGCACCAGTGGTCCATCGGACATCCAGATGACCCAGTCTCCATCCTCC

CTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTCGTC

CGATTGGGACGACGTTAAGTTGGTACCAGCAGAAACCAGGGAAGCCCTA

AGCTCCTGATCTGGTTTGGTCCCGGTTGCAAAGTGGGGTCCCATCACGTTT

CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCA

ACCTGAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACG

ACGTTCCGCCAAGGGACCAAGGTGGAAATCAAACGGGCGGCCGAGAACA

AAAACCTCATCTCAGAAGAGGATCTGAATTAA

TABLE 5-continued

## Anti-serum albumin dAb (DOM7h) fusions

DOM7h-11-12/DOM1m-21-23 fusion DMS number 5516

Amino acid sequence (SEQ ID NO: 327)

EVQLLESGGGLVQPGGSLRLSCAASGFTFNRYSMGWLRQAPGKGLEWVSRIDS

YGRGTYIEDPVKGRFSISRDN SKNTLYLQMNSLRAEDTAVYYCAKISQFGSNA

FDYWGQGTQVTVSSASTSGPSDIQMTQSPSSLSASVGD RVTITCRASRP IGTMLS

WYQQKPKGKAPKLLILFGSRLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCA

QAGTHPTTFGQGTKVEIKR

Amino acid plus nucleotide plus myc tag sequence (SEQ ID NO: 328)

EVQLLESGGGLVQPGGSLRLSCAASGFTFNRYSMGWLRQAPGKGLEWVSRIDS

YGRGTYIEDPVKGRFSISRDN SKNTLYLQMNSLRAEDTAVYYCAKISQFGSNA

FDYWGQGTQVTVSSASTSGPSDIQMTQSPSSLSASVGD RVTITCRASRP IGTMLS

WYQQKPKGKAPKLLILFGSRLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCA

QAGTHPTTFGQGTKVEIKRAAAEQKLI SEEDLN

Nucleotide sequence (SEQ ID NO: 329)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCC

CTGCGTCTCCTCTGTGCAGCCTCCGGATTCACCTTTAATAGGTATAGTATGG

GGTGGCTCCGCCAGGCTCCAGGAAGGGTCTAGAGTGGGTCTCACGGATTG

ATTCTTATGGTCGTGGTACATACTACGAAGACCCCGTAAGGGCCGGTTCA

GCATCTCCCGGACAATCCAAGAACACGCTGTATCTGCAATGAACAGCC

TGCGTGCCGAGGACACCGCGTATATTACTGTGCGAAAATTTCTCAGTTTGG

GTCAAATGCGTTTGACTACTGGGGTCAGGGAACCCAGGTCACCGTCTCGAG

CGCTAGCACCAGTGGTCCATCGGACATCCAGATGACCCAGTCTCCATCCTCC

CTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTCGTC

CGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCAGGGAAAGCCCTA

AGCTCCTGATCTTGTGGTTCCCGGTTGCAAAGTGGGGTCCCATCACGTTT

CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCA

ACCTGAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACG

ACGTTCCGCCAAGGGACCAAGGTGGAAATCAAACGG

Nucleotide plus myc tag sequence (SEQ ID NO: 330)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCC

CTGCGTCTCCTCTGTGCAGCCTCCGGATTCACCTTTAATAGGTATAGTATGG

GGTGGCTCCGCCAGGCTCCAGGAAGGGTCTAGAGTGGGTCTCACGGATTG

ATTCTTATGGTCGTGGTACATACTACGAAGACCCCGTAAGGGCCGGTTCA

GCATCTCCCGGACAATCCAAGAACACGCTGTATCTGCAATGAACAGCC

TGCGTGCCGAGGACACCGCGTATATTACTGTGCGAAAATTTCTCAGTTTGG

GTCAAATGCGTTTGACTACTGGGGTCAGGGAACCCAGGTCACCGTCTCGAG

CGCTAGCACCAGTGGTCCATCGGACATCCAGATGACCCAGTCTCCATCCTCC

CTGTCTGCATCTGTAGGAGACCGTGTACCATCACTTGCCGGGCAAGTCGTC

CGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCAGGGAAAGCCCTA

AGCTCCTGATCTTGTGGTTCCCGGTTGCAAAGTGGGGTCCCATCACGTTT

CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCA

ACCTGAAGATTTTGCTACGTACTACTGTGCGCAGGCTGGGACGCATCCTACG

TABLE 5-continued

Anti-serum albumin dAb (DOM7h) fusions

ACGTTTCGGCCAAGGACCAAGGTGGAAATCAAACGGGCGGCCGAGAACA

AAAACCTCATCTCAGAAGAGGATCTGAATTAA

DOM7h-11-15/DOM1m-21-23 fusion DMS number 5517

Amino acid sequence (SEQ ID NO: 331)

EVQLLESGGGLVQPGGSLRLSCAASGFTFNRYSMGWLRQAPGKGLEWVSRIDS

YGRGTYIEDPVKGRFSISRDN SKNTLYLQMNSLRAEDTAVYYCAKISQFGSNA

FDYWGGTQVTVSSASTSGPSDIQMTQSPSSLSASVGD RVTITCRASRP IGTMLS

WYQQKPKGKAPKLLILAFSRLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCA

QAGTHPTTFGQGTKVEIKR

Amino acid plus nucleotide plus myc tag sequence (SEQ ID NO: 332)

EVQLLESGGGLVQPGGSLRLSCAASGFTFNRYSMGWLRQAPGKGLEWVSRIDS

YGRGTYIEDPVKGRFSISRDN SKNTLYLQMNSLRAEDTAVYYCAKISQFGSNA

FDYWGGTQVTVSSASTSGPSDIQMTQSPSSLSASVGD RVTITCRASRP IGTMLS

WYQQKPKGKAPKLLILAFSRLQSGVPSRFSGSGSGTDFTLTIS SLQPEDFATYYCA

QAGTHPTTFGQGTKVEIKRAAEQKLI SEEDLN

Nucleotide sequence (SEQ ID NO: 333)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCC

CTGCGTCTCTCCTGTGCAGCCTCCGGATTACCTTTAATAGGTATAGTATGG

GGTGGCTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGGATTG

ATTCTTATGGTCGTGGTACATACTACGAAGACCCCGTGAAGGGCCGGTTCA

GCATCTCCCGGACAATCCAAGAACACGCTGTATCTGCAAATGAACAGCC

TGCGTGCCGAGGACACCGCGTATATTACTGTGCGAAAATTTCTCAGTTTGG

GTCAAATGCGTTTGACTACTGGGGTCAGGGAACCCAGGTCACCGTCTCGAG

CGCTAGCACCAGTGGTCCATCGGACATCCAGATGACCCAGTCTCCATCCTCC

CTGTCTGCATCTGTAGGAGACCGTGTCAACCATCACTTGCCGGCAAGTCGTC

CGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCAGGGAAGCCCTA

AGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCACGTTTC

AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA

CCTGAAGATTTTGTACTACTACTGCGCGCAGGCTGGGACGCATCCTACGA

CGTTCGGCCAAGGACCAAGGTGGAAATCAAACGG

Nucleotide plus myc tag sequence (SEQ ID NO: 334)

GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCC

CTGCGTCTCTCCTGTGCAGCCTCCGGATTACCTTTAATAGGTATAGTATGG

GGTGGCTCCGCCAGGCTCCAGGGAAGGGTCTAGAGTGGGTCTCACGGATTG

ATTCTTATGGTCGTGGTACATACTACGAAGACCCCGTGAAGGGCCGGTTCA

GCATCTCCCGGACAATCCAAGAACACGCTGTATCTGCAAATGAACAGCC

TGCGTGCCGAGGACACCGCGTATATTACTGTGCGAAAATTTCTCAGTTTGG

GTCAAATGCGTTTGACTACTGGGGTCAGGGAACCCAGGTCACCGTCTCGAG

CGCTAGCACCAGTGGTCCATCGGACATCCAGATGACCCAGTCTCCATCCTCC

CTGTCTGCATCTGTAGGAGACCGTGTCAACCATCACTTGCCGGCAAGTCGTC

CGATTGGGACGATGTTAAGTTGGTACCAGCAGAAACCAGGGAAGCCCTA

TABLE 5-continued

Anti-serum albumin dAb (DOM7h) fusions
AGCTCCTGATCCTTGCTTTTCCCGTTTGCAAAGTGGGGTCCCATCACGTTTC
AGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAA
CCTGAAGATTTTGCTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGA
CGTTCGGCCAAGGGACCAAGGTGGAAATCAAACGGGCGGCCGAGAACAA
AAACTCATCTCAGAAGAGGATCTGAATTA

where a myc-tagged molecule is indicated in this table, this was the version used in PK studies in the examples. Where no myc-tagged sequences are given, the PK studies in the examples were not done with myc-tagged material, ie, the studies were done with the non-tagged constructs shown.

## EXEMPLIFICATION

All numbering in the experimental section is according to Kabat (Kabat, E. A. National Institutes of Health (US) & Columbia University. Sequences of proteins of immunological interest, edn 5 (US Dept. Of Health and Human Services Public Health Service, National Institutes of Health, Bethesda, Md., 1991)).

Derivation of DOM7h-11 and DOM7h-14 variants is described. DOM7h-11 variants are not according to the invention.

## Example 1

## Vk Affinity Maturation

## Selections:

HSA (Human Serum Albumin) and RSA (Rat Serum Albumin) antigens were obtained from Sigma (essentially fatty acid free, ~99% (agarose gel electrophoresis), lyophilized powder Cat. No. A3782 and A6414 respectively)

Biotinylated products of above two antigens were made by using EZ Link Sulfo-NHS-SS-Biotin (Pierce, Cat. No. 21331). Free biotin reagent was removed by passing the samples twice through PD10 desalting column followed by overnight dialysis against 1000x excess volume of PBS at 4°C. Resulting product was tested by mass spec and 1-2 biotins per molecule were observed.

## Affinity Maturation Libraries:

Both error-prone and CDR libraries were created using DOM7h-11 and DOM7h-14 parental dAbs (see WO2008/096158 for the sequences of DOM7h-11 and DOM7h-14). The CDR libraries were generated in the pDOM4 vector and the error prone libraries were generated in the pDOM33 vector (to allow for selection with or without protease treatment). Vector pDOM4, is a derivative of the Fd phage vector in which the gene III signal peptide sequence is replaced with the yeast glycolipid anchored surface protein (GAS) signal peptide. It also contains a c-myc tag between the leader sequence and gene III, which puts the gene III back in frame. This leader sequence functions well both in phage display vectors but also in other prokaryotic expression vectors and can be universally used. pDOM33 is a modified version of the pDOM4 vector where the c-myc tag has been removed which renders the dAb-phage fusion resistant to the protease trypsin.

This allows the use of trypsin within the phage selection to select for dAbs that are more protease stable (see WO2008149143).

For error-prone maturation libraries, plasmid DNA encoding the dAb to be matured was amplified by PCR, using the GENEMORPH® II RANDOM MUTAGENESIS KIT (random, unique mutagenesis kit, Stratagene). The product was digested with Sal I and Not I and used in a ligation reaction with cut phage vector pDOM33.

For the CDR libraries, PCR reactions were performed using degenerate oligonucleotides containing NNK or NNS codons to diversify the required positions in the dAb to be affinity matured. Assembly PCR was then used to generate a full length diversified insert. The insert was digested with Sal I and Not I and used in a ligation reaction with pDOM4 for mutagenesis of multiple residues and pDOM5 for mutagenesis of single residues. The pDOM5 vector is a pUC119-based expression vector where protein expression is driven by the LacZ promoter. A GAS 1 leader sequence (see WO 2005/093074) ensures secretion of isolated, soluble dAbs into the periplasm and culture supernatant of *E. coli*. dAbs are cloned SalI/NotI in this vector, which appends a myc tag at the C-terminus of the dAb. This protocol using SalI and Not I results in inclusion of an ST amino acid sequence at the N-terminus.

The ligation produced by either method was then used to transform *E. coli* strain TB1 by electroporation and the transformed cells plated on 2xTY agar containing 15 µg/ml tetracycline, yielding library sizes of >5x10<sup>7</sup> clones.

The error-prone libraries had the following average mutation rate and size: DOM7h-11 (2.5 mutations per dAb), size: 6.1x10<sup>8</sup>, DOM7h-14 (2.9 mutations per dAb), size: 5.4x10<sup>8</sup>.

Each CDR library has four amino acid diversity. Two libraries were generated for each of CDRs 1 and 3, and one library for CDR2. The positions diversified within each library are as follows (amino acids based on VK dummy DPK9 sequence):

	Library size	
	DOM7h-11	DOM7h-14
1 - Q27, S28, S30, S31 (CDR1)	8.8 × 10 <sup>7</sup>	5.8 × 10 <sup>7</sup>
2 - S30, S31, Y32, N34 (CDR1)	4.6 × 10 <sup>8</sup>	4.2 × 10 <sup>8</sup>
3 - Y49, A50, A51, S53 (CDR2)	3.9 × 10 <sup>8</sup>	2.4 × 10 <sup>8</sup>
4 - Q89, S91, Y92, S93 (CDR3)	1.8 × 10 <sup>8</sup>	2.5 × 10 <sup>8</sup>
5 - Y92, Y93, T94, N96 (CDR3)	4.0 × 10 <sup>8</sup>	3.3 × 10 <sup>8</sup>

## Selection Strategies

Three phage selection strategies were adopted for Vκ 5  
AlbudAb™ (anti-serum albumin dAb) affinity maturation:

## 1) Selections against HSA only:

Three rounds of selection against HSA were carried out.

The error prone libraries and each CDR library were selected as an individual pool in all rounds. The first round of selection was performed against HSA passively coated onto an immunotube at 1 mg/ml. Round 2 was performed against 100 nM HSA and round 3 against 10 nM (CDR selections) or 20 or 100 nM (Error prone selections) HSA, both as soluble selections followed by a fourth round of selection with the error prone libraries against 1.5 nM HSA as a soluble selection. The error prone libraries were eluted with 0.1M glycine pH 2.0 before neutralisation with 1M Tris pH 8.0 and the CDR libraries were eluted with 1 mg/ml trypsin before infection into log phase TG1 cells. The third round of each selection was subcloned into pDOM5 for screening. Soluble selections used biotinylated HSA.

## 2) Trypsin Selections Against HSA:

In order to select dAbs with increased protease resistance compared to the parental clone and with potentially improved biophysical properties, trypsin was used in phage selections (see WO2008149143). Four rounds of selection were performed against HSA. The first round of selection of error prone libraries was performed against passively coated HSA at 1 mg/ml without trypsin; the second round against passively coated HSA at 1 mg/ml with 20 µg/ml trypsin for 1 hour at 37° C.; the third round selection was performed by soluble selection using biotinylated HSA against 100 nM HSA with 20 µg/ml or 100 µg/ml trypsin for 1 hour at 37° C. The final round of selection was performed by soluble selection using biotinylated HSA against 100 nM HSA with 100 µg/ml trypsin overnight at 37° C.

## 3) Cross-over selections against HSA (round 1) and RSA (rounds 2-4):

The first round selection was carried out against 1 mg/ml passively coated HSA or 1 µM HSA (soluble selection), followed by a further three rounds of soluble selections against biotinylated RSA at concentrations of 1 µM for round 1, 100 nM for round 2 and 20 nM, 10 nM or 1 nM for round 3.

## Screening Strategy and Affinity Determination:

In each case after selection a pool of phage DNA from the appropriate round of selection is prepared using a QIAfilter midiprep kit (Qiagen), the DNA is digested using the restriction enzymes SalI and NotI and the enriched V genes are ligated into the corresponding sites in pDOM5 the soluble expression vector which expresses the dAb with a myc tag (see PCT/EP2008/067789). The ligated DNA is used to electro-transform *E. coli* HB 2151 cells which are then grown overnight on agar plates containing the antibiotic carbenicillin. The resulting colonies are individually assessed for antigen binding. In each case at least 96 clones were tested for binding to HSA, CSA (*Cynomolgus* monkey Serum Albumin), MSA (mouse serum albumin) and RSA by BIAcore™ (surface plasmon resonance). MSA antigen was obtained from Sigma (essentially fatty acid free, ~99% (agarose gel electrophoresis), lyophilized powder Cat. No. A3559) and CSA was purified from *Cynomolgus* serum albumin using prometec blue resin (Amersham). Soluble dAb fragments were produced in bacterial culture in ONEX culture media (Novagen)

overnight at 37° C. in 96 well plates. The culture supernatant containing soluble dAb was centrifuged and analysed by BIAcore for binding to high density HSA, CSA, MSA and RSA CM5 chips. Clones were found to bind to all these species of serum albumin by off-rate screening. The clones were sequenced revealing unique dAb sequences.

The minimum identity to parent (at the amino acid level) of the clones selected was 97.2% (DOM7h-11-3: 97.2%, DOM7h-11-12: 98.2%, DOM7h-11-15: 96.3%, DOM7h-11-18: 98.2%, DOM7h-11-19: 97.2%)

The minimum identity to parent (at the amino acid level) of the clones selected was 96.3% (DOM7h-14-10: 96.3%, DOM7h-14-18: 96.3%, DOM7h-14-19: 98.2%, DOM7h-14-28: 99.1%, DOM7h-14-36: 97.2%)

Unique dAbs were expressed as bacterial supernatants in 2.5 L shake flasks in Onex media at 30° C. for 48 hrs at 250 rpm. dAbs were purified from the culture media by absorption to protein L agarose followed by elution with 10 mM glycine pH2.0. Binding to HSA, CSA, MSA and RSA by BIAcore was confirmed using purified protein at 3 concentrations 1 µM, 500 nM and 50 nM. To determine the binding affinity ( $K_D$ ) of the AlbudAbs to each serum albumin; purified dAbs were analysed by BIAcore over albumin concentration range from 5000 nM to 39 nM (5000 nM, 2500 nM, 1250 nM, 625 nM, 312 nM, 156 nM, 78 nM, 39 nM).

TABLE 6

AlbudAb	Affinity ( $K_D$ ) to SA (nM)	Kd	Ka
	Rat		
DOM7h-14	60	2.095E-01	4.00E+06
DOM7h-14-10	4	9.640E-03	4.57E+06
DOM7h-14-18	410	2.275E-01	5.60E+05
DOM 7h-14-19	890	2.870E-01	3.20E+05
DOM 7h-14-28	45 (140)	7.0E-02 (1.141e-1)	2.10E+06 (8.3e5)
DOM 7h-14-36	30 (6120)	2.9E-02 (5.54e-2)	1.55E+06 (9e3)
DOM 7h-11	2100	1.00E-01	4.80E+04
DOM 7h-11-3	10000 (88000)	(7.18e-1)	(8.11e3)
DOM 7h-11-12	200	5.22E-01	2.76E+06
DOM 7h-11-15	20	2.10E-02	1.10E+06
DOM 7h-11-18	80 (29000)	6.0E-02	1.64E+06 (1.3e4)
DOM 7h-11-19	28 (17000)	9.1e-02 (1.4e-1)	9.80E+05 (8.1e3)
	Cyno		
DOM 7h-14	66	9.65E-02	1.50E+06
DOM 7h-14-10	9	1.15E-02	1.60E+06
DOM 7h-14-18	180	1.05E-01	6.30E+5
DOM 7h-14-19	225	1.56E-01	7.00E+05
DOM 7h-14-28	66 (136)	1.3E-01 (1.34e-1)	2.50E+06 (9.8e5)
DOM 7h-14-36	35 (7830)	1.9E-02 (1.1e-1)	9.80E+06 (1.43e4)
DOM 7h-11	1000	6.82E-01	8.00E+05
DOM 7h-11-3	670 (200)	9.6E-02 (1.5e-1)	2.90E+05 (7.26e5)
DOM 7h-11-12	≥6000	5.57E-03	5.80E+06
DOM 7h-11-15	3	1.36	2.25E+05
DOM 7h-11-18	10000 (65000)	(4.8e-1)	(7.3e3)
DOM 7h-11-19	≥10000 (375000)	(6.2e-1)	(1.7e3)
	Mouse		
DOM 7h-14	12	4.82E-02	4.10E+06
DOM 7h-14-10	30	3.41E-02	1.29E+06
DOM 7h-14-18	65	9.24E-02	2.28E+06
DOM 7h-14-19	60	5.76E-02	1.16E+06
DOM 7h-14-28	26 (31)	3.4E-02 (7.15e-2)	1.60E+06 (2.28e6)

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TABLE 6-continued

AlbudAb	Affinity ( $K_D$ ) to SA (nM)	$K_d$	$K_a$
DOM 7h-14-36	35 (33)	2.3E-02 (7.06e-2)	8.70E+05 (2.11e6)
DOM 7h-11	5000	9.00E-01	
DOM 7h-11-3	$\geq 10000$ (36000)	(6.12e-1)	(1.67e4)
DOM 7h-11-12	130	1.89E-01	1.53E+06
DOM 7h-11-15	10	9.40E-03	1.10E+06
DOM 7h-11-18	150 (1600)	2.4E-02 (6.23e-2)	4.40E+05 (4e4)
DOM 7h-11-19	100 (18000)	3.7E-02 (8.8e-2)	1.40E+06 (4.9e3)
	Human		
DOM 7h-14	33	4.17E-02	1.43E+06
DOM 7h-14-10	12	1.39E-02	1.50E+06
DOM 7h-14-18	280	3.39E-02	1.89E+05
DOM 7h-14-19	70	5.25E-02	8.26E+05
DOM 7h-14-28	30 (8260)	3.3E-02 (5.6e-2)	1.24E+06 (6.78e3)
DOM 7h-14-36	28 (1260)	2.4E-02 (6.7e-2)	1.23E+06 (5.4e4)
DOM 7h-11	2800	6.41E-01	7.00E+05
DOM 7h-11-3	32 (130)	1.6E-02 (2.35e-2)	6.50E+05 (1.86e5)
DOM 7h-11-12	350	4.13E-01	1.26E+06
DOM 7h-11-15	1	1.84E-03	2.00E+06
DOM 7h-11-18	36 (32000)	5.1E-02 (2.7e-1)	3.40E+06 (8.39e3)
DOM 7h-11-19	65 (38000)	1.1E-01 (2.09e-1)	1.80E+06 (5.4e3)

\*: values in brackets were derived from a second, independent SPR experiment.

All DOM7h-14 derived variants are cross-reactive to mouse, rat, human and cyno serum albumin. DOM7h-14-10

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has improved affinity to rat, cyno and human serum albumin compared to parent. DOM7h-14-28 has an improved affinity to RSA. DOM7h-14-36 has an improved affinity to RSA, CSA and MSA.

5 DOM7h-11-3 has improved affinity to CSA and HSA. DOM7h-11-12 has improved affinity to RSA, MSA and HSA. DOM7h-11-15 has improved affinity to RSA, MSA, CSA and HSA. DOM7h-11-18 and DOM7h-11-19 have improved affinity to RSA, MSA and HSA.

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## Example 3

## Origins of Key DOM7h-11 Lineage Clones

15 DOM7h-11-3: From affinity maturation performed against HSA using the CDR2 library (Y49, A50, A51, S53), round 3 output 10 nM HSA

DOM7h-11-12: From affinity maturation performed against HSA using the error prone library, round 3 outputs (100 nM, HSA) with 100 ug/ml trypsin.

20 DOM7h-11-15: From cross-over selections performed against HSA as round 1 followed by additional 3 rounds of selections against RSA using the CDR2 library (Y49, A50, A51, S53) at round 3 selection with 1 nM of RSA.

25 DOM7h-11-18 From cross-over selections performed against HSA as round 1 followed by additional 3 rounds of selections against RSA using the error prone library, round 3 output at 20 nM of RSA

30 DOM7h-11-19 From cross-over selections performed against HSA as round 1 followed by additional 3 rounds of selections against RSA using the error prone library, round 3 output at 5 nM of RSA

TABLE 7

CDR sequences (according to Kabat; ref. as above)			
AlbudAb	CDR		
	CDR1	CDR2	CDR3
DPK9 Vk dummy	SQSISSYLN (SEQ ID NO: 335)	YAASSLQS (SEQ ID NO: 336)	QQSYSTPNT (SEQ ID NO: 337)
DOM7h-11	SRPIGTTLS (SEQ ID NO: 338)	WFGSRLQS (SEQ ID NO: 339)	AQAGTHPTT (SEQ ID NO: 340)
DOM7h-11-12	SRPIGTMLS (SEQ ID NO: 341)	LFGSRLQS (SEQ ID NO: 342)	AQAGTHPTT (SEQ ID NO: 343)
DOM 7h-11-15	SRPIGTMLS (SEQ ID NO: 344)	LAFSRLQS (SEQ ID NO: 345)	AQAGTHPTT (SEQ ID NO: 346)
DOM 7h-11-18	SRPIGTMLS (SEQ ID NO: 347)	WFGSRLQS (SEQ ID NO: 348)	AQAGTHPTT (SEQ ID NO: 349)
DOM 7h-11-19	SRPIGTMLS (SEQ ID NO: 350)	LFGSRLQS (SEQ ID NO: 351)	AQTGTHPTT (SEQ ID NO: 352)
DOM 7h-11-3	SRPIGTTLS (SEQ ID NO: 353)	LWFSRLQS (SEQ ID NO: 354)	AQAGTHPTT (SEQ ID NO: 355)

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## Example 4

## Origins of Key DOM7h-14 Lineage Clones

DOM7h-14-19: From affinity maturation performed against HSA using the error prone library, round 3 outputs (100 nM, HSA) with 100 ug/ml trypsin.

DOM7h-14-10, DOM7h-14-18, DOM7h-14-28, DOM7h-14-36: From affinity maturation performed against HSA using CDR3 library (Y92, Y93, T94, N96), round 3 output.

TABLE 8

CDR sequences (according to Kabat; ref. as above)			
AlbudAb	CDR		
	CDR1	CDR2	CDR3
DPK9 Vk dummy	SQSISSYLN (SEQ ID NO: 335)	YAASSLQS (SEQ ID NO: 336)	QQSYSTPNT (SEQ ID NO: 337)
DOM 7h-14	SQWIGSQLS (SEQ ID NO: 356)	MWRSSLQS (SEQ ID NO: 357)	AQGAALPRT (SEQ ID NO: 358)
DOM 7h-14-10	SQWIGSQLS (SEQ ID NO: 359)	MWRSSLQS (SEQ ID NO: 360)	AQGLRHPKT (SEQ ID NO: 361)
DOM 7h-14-18	SQWIGSQLS (SEQ ID NO: 362)	MWRSSLQS (SEQ ID NO: 363)	AQGLMKPMT (SEQ ID NO: 364)
DOM 7h-14-19	SQWIGSQLS (SEQ ID NO: 365)	MWRSSLQS (SEQ ID NO: 366)	AQGAALPRT (SEQ ID NO: 367)
DOM 7h-14-28	SQWIGSQLS (SEQ ID NO: 368)	MWRSSLQS (SEQ ID NO: 369)	AQGAALPKT (SEQ ID NO: 370)
DOM 7h-14-36	SQWIGSQLS (SEQ ID NO: 371)	MWRSSLQS (SEQ ID NO: 372)	AQGFKKPRT (SEQ ID NO: 373)

## Example 5

## Expression and Biophysical Characterisation

The routine bacterial expression level in 2.5 L shake flasks was determined following culture in Onex media at 30° C. for 48 hrs at 250 rpm. The biophysical characteristics were determined by SEC MALLS and DSC.

SEC MALLS (size exclusion chromatography with multi-angle-LASER-light-scattering) is a non-invasive technique for the characterizing of macromolecules in solution. Briefly, proteins (at concentration of 1 mg/mL in buffer Dulbecco's PBS at 0.5 ml/min are separated according to their hydrodynamic properties by size exclusion chromatography (column: TSK3000 from TOSOH Biosciences; S200 from Pharmacia). Following separation, the propensity of the protein to scatter light is measured using a multi-angle-LASER-light-scattering (MALLS) detector. The intensity of the scattered light while protein passes through the detector is measured as a function of angle. This measurement taken together with the protein concentration determined using the refractive index (RI) detector allows calculation of the molar mass using appropriate equations (integral part of the analysis software Astra v.5.3.4.12).

DSC (Differential Scanning calorimetry): briefly, the protein is heated at a constant rate of 180° C./hrs (at 1 mg/mL in

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PBS) and a detectable heat change associated with thermal denaturation measured. The transition midpoint ( $_{app}T_m$ ) is determined, which is described as the temperature where 50% of the protein is in its native conformation and the other 50% is denatured. Here, DSC determined the apparent transition midpoint (appTm) as most of the proteins examined do not fully refold. The higher the Tm, the more stable the molecule. Unfolding curves were analysed by non-2-state equations. The software package used was Origin® v7.0383.

40

TABLE 9

AlbudAb	Biophysical parameters	
	SEC MALLS	DSC Tm (° C.)
DOM7h-14	M	60
DOM 7h-14-10	M	59
DOM 7h-14-18	M	58
DOM 7h-14-19	M	59
DOM 7h-14-28	M	58.3/60.2
DOM 7h-14-36	M	59.2
DOM 7h-11	M	66.9-72.2
DOM 7h-11-3	M (95%)*	66.6/70.5
DOM 7h-11-12	M (<2% D)	71.7
DOM 7h-11-15	M (<5% D)	58.5-60.5
DOM 7h-11-18	M (98%)	58.9/65.8
DOM 7h-11-19	M	71.8/76.6

\*in one other trial, monomer was primarily seen by SEC MALLS, although lower than 95%

We observed expression levels for all clones in Table 9 in the range from 15 to 119 mg/L in *E. coli*.

For DOM7h-14 and DOM7h-11 variants, favorable biophysical parameters (monomeric in solution as determined by SEC MALLS and appTm of >55° C. as determined by DSC) and expression levels were maintained during affinity maturation. Monomeric state is advantageous because it avoids dimerisation and the risk of products that may cross-link targets such as cell-surface receptors.

Determination of Serum Half Life in Rat, Mouse and *Cynomolgus* Monkey

AlbudAbs DOM7h-14-10, DOM7h-14-18, DOM7h-14-19, DOM7h-11, DOM7h11-12 and DOM7h-11-15 were cloned into the pDOM5 vector. For each AlbudAb™, 20-50 mg quantities were expressed in *E. coli* and purified from bacterial culture supernatant using protein L affinity resin and eluted with 100 mM glycine pH2. The proteins were concentrated to greater than 1 mg/ml, buffer exchanged into PBS and endotoxin depleted using Q spin columns (Vivascience). For Rat pharmacokinetic (PK) analysis, AlbudAbs were dosed as single i.v injections at 2.5 mg/kg using 3 rats per compound. Serum samples were taken at 0.16, 1, 4, 12, 24, 48, 72, 120, 168 hrs. Analysis of serum levels was by anti-myc ELISA as per the method described below.

For Mouse PK, DOM7h-11, DOM7h11-12 and DOM7h-11-15 were dosed as single i.v injections at 2.5 mg/kg per dose group of 3 subjects and serum samples taken at 10 mins; 1 h; 8 h; 24 h; 48 h; 72 h; 96 h. Analysis of serum levels was by anti-myc ELISA as per the method described below.

For *Cynomolgus* monkey PK DOM7h-14-10 and DOM7h-11-15 were dosed as single i.v injections at 2.5 mg/kg into 3 female *Cynomolgus* monkeys per dose group and serum samples taken at 0.083, 0.25, 0.5, 1, 2, 4, 8, 24, 48, 96, 144, 192, 288, 336, 504 hrs. Analysis of serum levels was by anti-myc ELISA as per the method described below.

Anti-Myc ELISA Method

The AlbudAb concentration in serum was measured by anti-myc ELISA. Briefly, goat anti-myc polyclonal antibody (1:500; Abcam, catalogue number ab9132) was coated overnight onto Nunc 96-well Maxisorp plates and blocked with 5% BSA/PBS+1% tween. Serum samples were added at a range of dilutions alongside a standard at known concentrations. Bound myc-tagged AlbudAb was then detected using a rabbit polyclonal anti-Vk (1:1000; in-house reagent, bleeds were pooled and protein A purified before use) followed by an anti-rabbit IgG HRP antibody (1:10,000; Sigma, catalogue number A2074). Plates were washed between each stage of the assay with 3xPBS+0.1% Tween20 followed by 3xPBS. TMB (SureBlue TMB 1-Component Microwell Peroxidase Substrate, KPL, catalogue number 52-00-00) was added after the last wash and was allowed to develop. This was stopped with 1M HCl and the signal was then measured using absorbance at 450 nm.

From the raw ELISA data, the concentration of unknown samples was established by interpolation against the standard curve taking into account dilution factors. The mean concentration result from each time point was determined from replicate values and entered into WinNonLin analysis package (eg version 5.1 (available from Pharsight Corp., Mountain View, Calif. 94040, USA). The data was fitted using a non-compartmental model, where PK parameters were estimated by the software to give terminal half-lives. Dosing information and time points were selected to reflect the terminal phase of each PK profile.

TABLE 10

		Single AlbudAb™ PK				
		PK parameters				
Species	AlbudAb	Albumin K <sub>D</sub> (nM)	AUC h x µg/ml	CL ml/h/kg	t <sub>1/2</sub> h	V <sub>Z</sub> ml/kg
Rat	DOM7h-14*	60				
	DOM7h-14-10	4	2134.6	1.2	42.1	71.2
	DOM7h-14-18	410	617.3	4.1	38.4	228.1
	DOM7h-14-19	890	632.6	4.1	36.3	213.3
	DOM7h-11	2100	320.1	7.8	23.3	263.9
	DOM7h-11-12	200	398.7	6.4	35.5	321.2
	DOM7h-11-15	20	843.4	3.0	30.3	130.7
mouse	DOM7h-11	5000	304.7	8.2	18.3	216.8
	DOM7h-11-12	130	646.6	3.9	43.9	244.8
	DOM7h-11-15	10	499.2	5.0	33.7	243.4
Cyno	DOM7h-14*	66			217.5	
	DOM7h-14-10	9	6174.6	0.4	200.8	117.8
	DOM7h-11*	3300			135.1	
	DOM7h-11-15	3	4195	0.6	198.1	170.3

\*Historical data

Pharmacokinetic parameters derived from rat, mouse and *cynomolgus* monkey studies were fitted using a non-compartmental model. Key: AUC: Area under the curve from dosing time extrapolated to infinity; CL: clearance; t<sub>1/2</sub>: is the time during which the blood concentration is halved; V<sub>Z</sub>: volume of distribution based on the terminal phase.

DOM7h-11 12 and DOM7h-11-15 have an improved AUC and t<sub>1/2</sub> in rat and mouse compared to parent. DOM7h-11-15 also has an improved AUC and t<sub>1/2</sub> in cyno compared to parent. This improvement in AUC/t<sub>1/2</sub> correlates with an improved in vitro KD to serum albumin.

Example 7

AlbudAb™ IFN Fusions

Cloning and Expression

As well as single AlbudAbs, the affinity matured Vk AlbudAbs were linked to Interferon alpha 2b (IFNα2b) to determine whether a useful PK of the AlbudAb was maintained as a fusion protein.

Interferon Alpha 2b Amino Acid Sequence:

(SEQ ID NO: 374)  
 CDLPQTHSLGSRRTLMLLAQMRRISLFSCLKDRHDFGFPQEEFGNQPKA  
 ETIPVLHEMIQQIFNLFSTKDSAAWDETLLDKFYTELYQQLNDEACVI  
 QGVGVTEPLMKEDSILAVRKYFQRITLYLKEKKYSPCAWEVVRAEI  
 MRSFSLSTNLQESLSRKE

Interferon Alpha 2b Nucleotide Sequence:

(SEQ ID NO: 375)  
 TGTGATCTGCCTCAAACCCACAGCCTGGGTAGCAGGAGACCTTGATGCT  
 CCTGGCACAGATGAGGAGAATCTCTCTTTTCTCCTGCCTGAAGGACAGAC  
 ATGACTTTGGATTTCCTCCAGGAGGAGTTGGCAACCAGTTCAAAAGGCT  
 GAAACCATCCCTGTCTCCATGAGATGATCCAGCAGATCTTCAATCTCTT  
 CAGCACAAAGGACTCATCTGCTGCTTGGGATGAGACCCTCCTAGACAAAT  
 TCTACACTGAACTCTACCAGCAGCTGAATGACCTGGAAGCCTGTGTGATA  
 CAGGGGGTGGGGGTGACAGAGACTCCCTGTATGAAGGAGGACTCCATTC

-continued

TGGCTGTGAGGAAATACTTCCAAGAATCACTCTCTATCTGAAAGAGAAG  
 AAATACAGCCCTTGTGCCTGGGAGGTTGTCAGAGCAGAAATCATGAGAT  
 CTTTTTCTTTGTCAACAACTTGCAGAAAGTTTAAGAAGTAAGGAA

IFN $\alpha$ 2b was linked to the AlbuAb via a TVAAPS linker region (see WO2007085814). The constructs were cloned by SOE-PCR (single overlap extension according to the method of Horton et al. Gene, 77, p 61 (1989)). PCR amplification of the AlbuAb and IFN sequences were carried out separately using primers with a ~15 base pair overlap at the TVAAPS linker region. The primers used are as follows:—

IFN $\alpha$ 2b SOE fragment 5' (SEQ ID NO: 376)  
 GCCCGGATCCACCGGCTGTGATCTG  
 IFN $\alpha$ 2b SOE fragment 3' (SEQ ID NO: 377)  
 GGAGGATGGAGACTGGTTCATCTGGATGTC  
 Vk SOE fragment 5' (SEQ ID NO: 378)  
 GACATCCAGATGACCCAGTCTCCATCCTCC  
 Vk SOE fragment 3' to also introduce a myc tag (SEQ ID NO: 379)  
 GCGCAAGCTTTTATTAATTCAGATCCTCTTCTGAGATGAGTTTTTGTTC  
 TGGCGCCGCCGTTTGATTTCACCTTGGTCCC

The fragments were purified separately and subsequently assembled in a SOE (single overlap extension PCR extension) reaction using only the flanking primers.

IFN $\alpha$ 2b SOE fragment 5' (SEQ ID NO: 380)  
 GCCCGGATCCACCGGCTGTGATCTG

5 Vk SOE fragment 3' to also introduce a myc tag (SEQ ID NO: 381)  
 GCGCAAGCTTTTATTAATTCAGATCCTCTTCTGAGATGAGTTTTTGTTC  
 GCGCGCCGCCGTTTGATTTCACCTTGGTCCC

10 The assembled PCR product was digested using the restriction enzymes BamHI and HindIII and the gene ligated into the corresponding sites in the pDOM50, a mammalian expression vector which is a pTT5 derivative with an N-terminal V-J2-C mouse IgG secretory leader sequence to facilitate expression into the cell media.

15 Leader Sequence (Amino Acid):

METDTLLLVLLLVVPGSTG (SEQ ID NO: 382)

20 Leader Sequence (Nucleotide):

(SEQ ID NO: 383)  
 ATGGAGACCGACCCCTGCTGCTGTGGGTGCTGCTGTGGGTGCCCGG  
 25 ATCCACCGGGC

30 Plasmid DNA was prepared using QIAfilter megaprep (Qiagen). 1  $\mu$ g DNA/ml was transfected with 293-Fectin into HEK293E cells and grown in serum free media. The protein is expressed in culture for 5 days and purified from culture supernatant using protein L affinity resin and eluted with 100 mM glycine pH2. The proteins were concentrated to greater than 1 mg/ml, buffer exchanged into PBS and endotoxin depleted using Q spin columns (Vivascience).

TABLE 11

Interferon alpha 2b-AlbuAb sequences with and without myc-tag (as amino acid- and nucleotide sequence) The Interferon alpha 2b is N-terminal to the AlbuAb in the following fusions.				
	aa + myc	nt + myc	aa no tag	nt no tag
DMS7321	CDLPQTHSLGSRRT	TGCGACTTGCC	CDLPQTHSLG	TGCGACTTGCC
(IFN $\alpha$ 2b-	LMLLAQMRRISLFS	ACAGACACAT	SRRTLMLLA	ACAGACACAT
DOM7h-	CLKDRHDFGFPQE	AGTTTGGGATC	QMRRIISLFS	AGTTTGGGATC
14)	EFGNQPKAETIPV	AAGAAGAACA	LKDRHDFGFP	AAGAAGAACA
	LHEMIQQIFNLFST	TTGATGTTATT	QEBFGNQFQ	TTGATGTTATT
	KDSSAAWDETLDD	AGCACAAATG	KAETIPVLHE	AGCACAAATG
	KFYTELYQQLNDL	CGTAGAATTC	MIQIIFNLFS	CGTAGAATTC
	EACVIQGVGTETP	TTTGTCTCTT	TKDSSAAWD	TTTGTCTCTT
	LMKEDSILAVRKY	GTCTAAAGGAC	ETLLDKFYTE	GTCTAAAGGAC
	FQRITLYLKEKKYS	CGTCACGACTT	LYQQLNDLE	CGTCACGACT
	PCAWEVVRAEIMR	CGGATCCCTC	ACVIQGVGV	TCGGATCCCT
	SFSLSTNLQESLRS	AGGAAGAGTTT	TETPLMKEDS	CAGGAAGAGT
	KETVAAPSDIQMT	GAAACCAATT	ILAVRKYFQR	TTGGAAACCA
	QSPSSLSASVGDV	CCAAAAGCA	ITLYLKEKKY	ATTCAAAAAA
	TITCRASQWIGSQL	GAAACTATTC	SPCAWEVVR	GCAGAAACTA
	SWYQQKPKGAPKL	TGTCTTGACG	AEIMRSFSL	TTCCTGTCTTG
	LIMWRSSLQSGVPS	AAATGATCCAG	TNLQESLRSK	CACGAAATGA
	RFSGSGSQTDFTLT	CAAAATTC	ETVAAPSDIQ	TCCAGCAAATA
	ISSLQPEDFATYYC	TTTGTTTTCTA	MTQSPSSLSA	TTCAATTTGTT
	AQGAALPRTFGQG	CAAAGGACTC	SVGDRVITIC	TTCTACAAAGG
	TKVEIKR	ATCAGCCGCTT	RASQWIGSQL	ACTCATCAGCC
	<b>AAAEQKLISEEDL</b>	GGGATGAAAC	SWYQQKPKG	GCTTGGGATGA
<b>N*</b> (SEQ ID NO: 384)		TCTGTTAGATA	APKLLIMWR	AACTCTGTTAG
		AAATCTACACT	SSLQSGVPSR	ATAAATCTTAC
		GAATATATCA	FSGSGSDF	ACTGAACTATA
		ACAACGTAAAC	TLTISSLPED	TCAACAACGTAA
		GATCTAGAGGC	FATYYCAQG	ACGATCTAGA
		TTGCGTTATTC	AALPRTFGQ	GGCTTGCCTTA
		AGGGTGTAGG	GTKVEIKR	TTCAGGGTGTAA
		AGTTACTGAAA	(SEQ ID	GGAGTTACTGA

TABLE 11-continued

Interferon alpha 2b-AlbudAb sequences with and without myc-tag (as amino acid- and nucleotide sequence) The Interferon alpha 2b is N-terminal to the AlbudAb in the following fusions.				
aa + myc	nt + myc	aa no tag	nt no tag	
	CTCCCCTAATG NO: 386)		AACTCCCCTAA	
	AAAGAAGATT		TGAAAGAAGA	
	CAATTCAGCC		TTCAATTCAG	
	GTTAGAAAATA		CCGTTAGAAA	
	CTTTCAGCGTA		ATACTTTCAGC	
	TCACATTGTAT		GTATCACATTG	
	TTAAAGGAAA		TATTTAAAGGA	
	AGAAATACTCC		AAAGAAATAC	
	CCATGTGCATG		TCCCATGTGC	
	GGAGGTGGTTA		ATGGGAGGTG	
	GAGCAGAAAT		GTTAGAGCAG	
	TATGAGGTCCCT		AAATTATGAG	
	TCTCTCTTCT		GTCCTTCTCTC	
	ACGAATTTGCA		TTTCTACGAAT	
	AGAATCTTTGA		TTGCAAGAATC	
	GATCTAAGGA		TTGAGATCTA	
	AACCGTCGCTG		AGGAAACCGT	
	CTCCATCTGAC		CGCTGCTCCAT	
	ATCCAGATGAC		CTGACATCCAG	
	CCAGTCTCCAT		ATGACCCAGTC	
	CCTCCCTGTCT		TCCATCCTCCC	
	GCATCTGTAGG		TGTCTGCATCT	
	AGACCGTGTCA		GTAGGAGACC	
	CCATCACTTGC		GTGTCACCATC	
	CGGGCAGATC		ACTTGCCGGGC	
	AGTGGATTGGG		AAGTCAGTGG	
	TCTCAGTTATC		ATTGGGTCTCA	
	TTGGTACCAGC		GTATCTTGGT	
	AGAAACCAGG		ACCAGCAGAA	
	GAAAGCCCTTA		ACCAGGGAAA	
	AGCTCCTGATC		GCCCCAAGCT	
	ATGTGGCGTTC		CCTGATCATGT	
	CTCGTTGCAAA		GGCGTTCCTCG	
	GTGGGGTCCCA		TTGCAAAGTGG	
	TCACGTTTCAG		GGTCCCATCAC	
	TGGCAGTGGAT		GTTTCAGTGGC	
	CTGGGACAGAT		AGTGGATCTGG	
	TTCACTCTCAC		GACAGATTTCA	
	CATCAGCAGTC		CTCTCACCATC	
	TGCAACCTGAA		AGCAGTCTGCA	
	GATTTTGCTAC		ACCTGAAGATT	
	GTACTACTGTG		TTGCTACGTAC	
	CTCAGGGTGGC		TACTGTGCTCA	
	GCGTTGCCTAG		GGGTGCGGCG	
	GACGTTCCGCC		TTGCCTAGGAC	
	AAGGGACCAA		GTTCGGCCAAG	
	GGTGGAATC		GGACCAAGGT	
	<b>AAACGGGCGG</b>		GGAAATCAAA	
	<b>CCGCAGAAC</b>		CGG (SEQ ID	
	<b>AAAACCTCATC</b>		NO: 387)	
	<b>TCAGAAAGAGG</b>			
	<b>ATCTGAATTA</b>			
	<b>A</b> (SEQ ID			
	NO: 385)			
DMS732	CDLPQTHSLGSRRT	TGCGACTTGCC	CDLPQTHSLG	TGCGACTTGCC
(IFN $\alpha$ 2b-	LMLLAQMRRISLFS	ACAGACACAT	SRRTLMLLA	ACAGACACAT
DOM7h-	CLKDRHDFGFPQE	AGTTTGGGATC	QMRRI SLFSC	AGTTTGGGATC
14-10)	EFGNQFQKAETIPV	AAGAAGAACA	LKDRHDFGFP	AAGAAGAACA
	LHEMIQQIFNLFST	TTGATGTTATT	QEEFNGQFPQ	TTGATGTTATT
	KDSSAAWDELTD	AGCACAAATG	KAETIPVLHE	AGCACAAATG
	KFYTELYQQLNDL	CGTAGAATTTT	MIQQIFNLF	CGTAGAATTTT
	EACVIQGVGVETETP	TTTGTCTCTT	TKDSSAAWD	TTTGTCTCTT
	LMKEDSILAVRKY	GTCTAAAGGAC	ETLLDKFYTE	GTCTAAAGGAC
	QRIITLYLKEKKYS	CGTCACGACTT	LYQQLNDLE	CGTCACGACTT
	PCAWEVVRAEIMR	CGGATTCCTC	ACVIQGVGV	TCCGATTCCTC
	SFSLSTNLQESLRS	AGGAAGAGTTT	TETPLMKEDS	CAGGAAGAGT
	KETVAAPSDIQMT	GGAAACCAATT	ILAVRKYFQR	TTGGAACCA
	QSPSSLSASVGDV	CCAAAAAGCA	ITLYLKEKKY	ATTCAAAAA
	TITCRASQWIGSQL	GAAACTATTCC	SPCAWEVVR	GCAGAAACTA
	SWYQQKPGKAPKL	TGCTTGCACG	AEIMRSFSL	TTCCTGTCTTG
	LIMWRSSLQSGVPS	AAATGATCCAG	TNLQESLRSK	CACGAAATGA
	RFSGSGSDTDFLT	CAATATTCAA	ETVAAPSDIQ	TCCAGCAAATA

TABLE 11-continued

Interferon alpha 2b-AlbudAb sequences with and without myc-tag (as amino acid- and nucleotide sequence) The Interferon alpha 2b is N-terminal to the AlbudAb in the following fusions.			
aa + myc	nt + myc	aa no tag	nt no tag
ISSLQPEDFATYYC	TTTGTTTCTA	MTQSPSSLSA	TTCAATTGTT
AQGLRHPKTFGQG	CAAAGGACTC	SVGDRVITIC	TTCTACAAAGG
TKVEIKR	ATCAGCCGCTT	RASQWIGSQL	ACTCATCAGCC
<b>AAAEQKLISEEDL</b>	GGGATGAAAC	SWYQQKPGK	GCTTGGGATGA
<b>N*</b> (SEQ ID NO: 388)	TCTGTTAGATA	APKLLIMWR	AACTCTGTTAG
	AATTCTACACT	SSLQSGVPSR	ATAAATTCTAC
	GAACATATATCA	FSGSGSGTDF	ACTGAACTATA
	ACAACTGAAC	TLTISSLQPED	TCAACAACCTGA
	GATCTAGAGGC	FATYYCAQG	ACGATCTAGA
	TTGCGTTATTC	LRHPKTFGQ	GGCTTGCGTTA
	AGGGTGTAGG	GTKVEIKR	TTCAGGGTGTGA
	AGTTACTGAAA	(SEQ ID	GGAGTTACTGA
	CTCCCCTAATG	NO: 390)	AACTCCCCATA
	AAAGAAGATT		TGAAAGAAGA
	CAATTCAGCC		TTCAATTCTAG
	GTTAGAAAATA		CCGTTAGAAA
	CTTTCAGCGTA		ATACTTTCAGC
	TCACATTGTAT		GTATCACATTG
	TTAAAGGAAA		TATTTAAAGGA
	AGAAATACTCC		AAAGAAATAC
	CCATGTGCATG		TCCCCATGTGC
	GGAGGTGGTTA		ATGGGAGGTG
	GAGCAGAAAT		GTAGAGCAG
	TATGAGGTCCT		AAATTATGAG
	TCTCTCTTCT		GTCCCTCTCTC
	ACGAATTTGCA		TTTCTACGAAT
	AGAATCTTTGA		TTGCAAGAATC
	GATCTAAGGA		TTTGAGATCTA
	AACCGTCGCTG		AGGAAACCGT
	CTCCATCTGAC		CGTGCTCCAT
	ATCCAGATGAC		CTGACATCCAG
	CCAGTCTCCAT		ATGACCCAGTC
	CCTCCCTGTCT		TCCATCCTCCC
	GCATCTGTAGG		TGCTGCATCT
	AGACCGTGTC		GTAGGAGACC
	CCATCACTTGC		GTGTCACCATC
	CGGGCAAGTC		ACTTGCCGGGC
	AGTGGATTGGG		AAGTCAGTGG
	TCTCAGTTATC		ATTGGGTCTCA
	TTGGTACCAGC		GTTATCTTGGT
	AGAAACCAGG		ACCAGCAGAA
	GAAAGCCCTA		ACCAGGAAA
	AGCTCCTGATC		GCCCCAAGCT
	ATGTGGCGTTC		CCTGATCATGT
	CTCGTTGCAAA		GGCGTTCCCTG
	GTGGGTCCCA		TTGCAAAGTGG
	TCACGTTTCAG		GGTCCCATCAC
	TGGCAGTGGAT		GTTCAGTGGC
	CTGGGACAGAT		AGTGGATCTGG
	TTCACTCTCAC		GACAGATTTCA
	CATCAGCAGTC		CTCTCACCATC
	TGCAACCTGAA		AGCAGTCTGCA
	GATTTTGCTAC		ACCTGAAGATT
	GTACTACTGTG		TTGCTACGTAC
	CTCAGGGTTTG		TACTGTGCTCA
	AGGCATCCTAA		GGGTTTGAGGC
	GACGTTGCGCC		ATCCTAAGACG
	AAGGGACCAA		TTCGGCCAAGG
	GGTGGAAATC		GACCAAGGTG
	AAACGGGCGG		GAAATCAAAC
	<b>CCGCAGAACA</b>		GG (SEQ ID
	<b>AAAACATC</b>		NO: 391)
	<b>TCAGAAGAGG</b>		
	<b>ATCTGAATTA</b>		
	<b>A</b> (SEQ ID		
	NO: 389)		

TABLE 11-continued

Interferon alpha 2b-AlbudAb sequences with and without myc-tag (as amino acid- and nucleotide sequence) The Interferon alpha 2b is N-terminal to the AlbuDAb in the following fusions.			
	aa + myc	nt + myc	aa no tag nt no tag
DMS7323	CDLPQTHSLGSRRT	TGCGACTTGCC	CDLPQTHSLG TGCGACTTGCC
(IFN $\alpha$ 2b-	LMLLAQMRRISLFS	ACAGACACAT	SRRTLMLLA ACAGACACAT
DOM7h-	CLKDRHDFGFPQE	AGTTTGGGATC	QMRRISLFS ACAGACACAT
14-18)	EFGNQFQKAETIPV	AAGAAGAACA	LKDRHDFGFP AAGAAGAACA
	LHEMIQQIFNLFST	TTGATGTTATT	QEFGNQFQ TTGATGTTATT
	KDSSAAWDELTD	AGCACAAATG	KAETIPVLHE AGCACAAATG
	KFYTELYQQLNDL	CGTAGAATTC	MIQQIFNLFST CGTAGAATTC
	EACVIQGVVETEP	TTTGTCTCTT	TKDSSAAWD TTTGTCTCTT
	LMKEDSILAVRKY	GTCTAAAGGAC	ETLLDKFYTE GTCTAAAGGAC
	PQRITLYLKEKKYS	CGTCACGACT	LYQQLNDLE CCGTCACGACT
	PCAWEVVRAEIMR	CGGATTCCTC	ACVIQGVGV TCGGATTCCTC
	SFSLSTNLQESLRS	AGGAAGAGTTT	TETPLMKEDS CAGGAAGAGT
	KETVAAPSDIQMT	GGAAACCAATT	ILAVRKYRQR TTGGAACCA
	QSPSSLSASVGDV	CCAAAAAGCA	ITLYLKEKKY ATTCCAAAA
	TITCRASQWIGSQL	GAAACTATTC	SPCAWEVVR GCAGAAACTA
	SWYQQKPKGAPKL	TGCTTGACAG	AEIMRSFSLT TTCTGTCTTG
	LIMWRSSLQSGVPS	AAATGATCCAG	TNLQESLRSK CACGAAATGA
	RFSGSGSGTDFTLT	CAAAATATCAA	ETVAAPSDIQ TCCAGCAATA
	ISSLQPEDFATYYC	TTTGTTTTCTA	MTQSPSSLSA TTCAATTTGTT
	AQGLMKPMTFQG	CAAAGGACTC	SVGDRVTITC TTCTACAAAGG
	GTKVEIKRAAAEQ	ATCAGCCGCTT	RASQWIGSQL ACTCATCAGCC
	<b>KLISEEDLN*</b> (SEQ	GGGATGAAAC	SWYQQKPKG GCTTGGGATGA
	ID NO: 392)	TCTGTTAGATA	APKLLIMWR AACTCTGTTAG
		AATTCTACACT	SSLQSGVPSR ATAAATCTTAC
		GAACTATATCA	FSGSGSGTDF ACTGAACTATA
		ACAACGTAAC	TLTSSSQPED TCAACAACGTA
		GATCTAGAGGC	FATYYCAQG ACGATCTAGA
		TTGCGTTATTC	LMKPMTFGQ GGCTTGCGTTA
		AGGGGTGTTAG	GTKVEIKR TTCAGGGTGTGA
		AGTTACTGAAA (SEQ	ID NO: 394)
		CTCCCTAATG	NO: 394) AACTCCCTTAA
		AAAGAAGATT	TGAAAGAAGA
		CAATTCTAGCC	TTCAATCTTAG
		GTTAGAAAATA	CCGTTAGAAA
		CTTTCAGCGTA	ATACTTTCAGC
		TCACATTGTAT	GTATCACATTG
		TTAAAGGAAA	TATTTAAAGGA
		AGAAATACTCC	AAAGAAATAC
		CCATGTGCATG	TCCCATGTGC
		GGAGGTGGTTA	ATGGGAGGTG
		GAGCAGAAAT	GTTAGAGCAG
		TATGAGGTCCCT	AAATTATGAG
		TCTCTTTTCT	GTCTTCTCTC
		ACGAATTTGCA	TTTCTACGAAT
		AGAACTTTGA	TTGCAAGAATC
		GATCTAAGGA	TTTGAGATCTA
		AACCGTCGCTG	AGGAAACCGT
		CTCCATCTGAC	CGCTGCTCCAT
		ATCCAGATGAC	CTGACATCCAG
		CCAGTCTCCAT	ATGACCCAGTC
		CCTCCCTGTCT	TCCATCCTCCC
		GCATCTGTAGG	TGTCTGCATCT
		AGACCGTGTCA	GTAGGAGACC
		CCATCACTTGC	GTGTCACCATC
		CGGGCAAGTC	ACTTGCCGGGC
		AGTGGATTGGG	AAGTCAGTGG
		TCTCAGTTATC	ATTGGGTCTCA
		TTGGTACCAGC	GTTATCTTGGT
		AGAAACCAGG	ACCAGCAGAA
		GAAAGCCCTTA	ACCAGGGAAA
		AGCTCCGATC	GCCCCAAGCT
		ATGTGGCGTTC	CCTGATCATGT
		CTCGTTGCAAA	GGCGTTCCTCG
		GTGGGGTCCCA	TTGCAAGTGG
		TCACGTTTCAG	GGTCCCATCAC
		TGGCAGTGGAT	GTTTCAGTGGC
		CTGGGACAGAT	AGTGGATCTGG
		TTCACCTCAC	GACAGATTTCA
		CATCAGCAGTC	CTCTCACCATC
		TGCAACCTGAA	AGCAGTCTGCA
		GATTTTGCTAC	ACCTGAGATT
		GTACTACTGTG	TTGCTACGTAC
		CTCAGGGTCTT	TACTGTGCTCA

TABLE 11-continued

Interferon alpha 2b-AlbudAb sequences with and without myc-tag (as amino acid- and nucleotide sequence) The Interferon alpha 2b is N-terminal to the AlbudAb in the following fusions.			
aa + myc	nt + myc	aa no tag	nt no tag
	ATGAAGCCTAT		GGGTCTTATGA
	GACGTTCGGCC		AGCCTATGACG
	AAGGGACCAA		TTCGCCAAGG
	GGTGGAAATC		GACCAAGGTG
	AAACGGGCGG		GAAATCAAAC
	<b>CCGCAGAACA</b>		GG (SEQ ID
	<b>AAAACTCATC</b>		NO: 395)
	<b>TCAGAAGAGG</b>		
	<b>ATCTGAATTA</b>		
	<b>A</b> (SEQ ID		
	NO: 393)		
DMS7324	TGCGACTTGCC	CDLPQTHSLG	TGCGACTTGCC
(IFN $\alpha$ 2b-	ACAGACACAT	SRRLMMLLA	ACAGACACAT
DOM7h-	AGTTTGGGATC	QMRRISLFS	AGTTTGGGATC
14-19)	AAGAAGACA	LKDRHDFGFP	AAGAAGACA
	TTGATGTTATT	QEEFGNQFQ	TTGATGTTATT
	AGCACAAATG	KAETIPVLHE	AGCACAAATG
	CGTAGAATTC	MIQQIFNLFS	CGTAGAATTC
	TTTGTCTCTT	TKDSSAAWD	TTTGTCTCTT
	GTCTAAAGGAC	ETLLDKFYTE	GTCTAAAGGAC
	CGTCACGACT	LYQQLNDLE	CGTCACGACT
	CGGATTCCTC	ACVIQGVGV	TCGGATTCCTC
	AGGAAGAGTTT	TETPLMKEDS	CAGGAAGAGT
	GGAAACCAATT	ILAVRKYPQR	TTGGAACCA
	CCAAAAAGCA	ITLYLKEKKY	ATTCCAAAAA
	GAAACTATTC	SPCAWEVVR	GCAGAAACTA
	TGTCTTGACAG	AEIMRSFSL	TTCTGTCTTG
	AAATGATCCAG	TNLQESLRSK	CACGAAATGA
	CAAAATATCAA	ETVAAPSDIQ	TCCAGCAATA
	TTTGTCTCTA	MTQSPSSLSA	TTCAATTTGTT
	CAAAGGACTC	SVGDRVTISC	TTCTACAAAGG
	ATCAGCCGCTT	RASQWIGSQL	ACTCATCAGCC
	GGGATGAAAC	SWYQKPGE	GCTTGGGATGA
	TCTGTAGATA	APKLLIMWR	AACTCTGTTAG
	AATTCTACACT	SSLQSGVPSR	ATAAATTTCTAC
	GAACTATATCA	FSGSGSGTDF	ACTGAACTATA
	ACAACCTGAAC	TLTISSLQPED	TCAACAACCTGA
	GATCTAGAGGC	FATYYCAQG	ACGATCTAGA
	TTGCGTTATTC	AALPRTFGQ	GGCTTGCGTTA
	AGGGTGTAGG	GTKVEIKR	TTCAGGGTGTGA
	AGTTACTGAAA	(SEQ ID	GGAGTTACTGA
	CTCCCTAATG	NO: 398)	AACTCCCTTAA
	AAAGAAGATT		TGAAAGAAGA
	CAATCTAGCC		TTCAATTTCTAG
	GTTAGAAAATA		CCGTTAGAAA
	CTTTCAGCGTA		ATACTTTCAGC
	TCACATTGTAT		GTATCACATTG
	TTAAAGGAAA		TATTTAAAGGA
	AGAAATACTCC		AAAGAAATAC
	CCATGTGCATG		TCCCATGTGC
	GGAGGTGGTTA		ATGGGAGGTG
	GAGCAGAAAT		GTTAGAGCAG
	TATGAGGTCCCT		AAATTATGAG
	TCTCTCTTCT		GTCTTCTCTC
	ACGAATTTGCA		TTTCTACGAAT
	AGAACTTTGA		TTGCAAGAATC
	GATCTAAGGA		TTTGAGATCTA
	AACCGTCGCTG		AGGAAACCGT
	CTCCATCTGAC		CGCTGCTCCAT
	ATCCAGATGAC		CTGACATCCAG
	CCAGTCTCCAT		ATGACCCAGTc
	CCTCCCTGTCT		TCCATCCTCCC
	GCATCTGTAGG		TGTCTGCATCT
	AGACCGTGTCA		GTAGGAGACC
	CCATCTCTTGC		GTGTCAACCATC
	CGGCAAGTC		TCTTGCCGGGC
	AGTGGATTGGG		AAGTCAGTGG
	TCTCAGTTATC		ATTGGGTCTCA
	TTGGTACCAGC		GTTATCTTGGT
	AGAAACCAGG		ACCAGCAGAA
	GGAAAGCCCTA		ACCAGGGGAA
	AGCTCCTGATC		GCCCCAAGCT

TABLE 11-continued

Interferon alpha 2b-AlbudAb sequences with and without myc-tag (as amino acid- and nucleotide sequence) The Interferon alpha 2b is N-terminal to the AlbudAb in the following fusions.			
aa + myc	nt + myc	aa no tag	nt no tag
	ATGTGGCGTTC		CCTGATCATGT
	CTCGTTGCAAA		GGCGTTCCTCG
	GTGGGGTCCCA		TTGCAAAGTGG
	TCACGTTTCAG		GGTCCCATCAC
	TGGCAGTGGAT		GTTTCAGTGGC
	CTGGGACAGAT		AGTGGATCTGG
	TTCACTCTCAC		GACAGATTTCA
	CATCAGCAGTC		CTCTCACCATC
	TGCAACCTGAA		AGCAGTCTGCA
	GATTTTGCTAC		ACCTGAAGATT
	GTACTACTGTG		TTGCTACGTAC
	CTCAGGGTGCG		TACTGTCTCA
	GCGTTCCTAG		GGGTGCGGCG
	GACGTTGCGCC		TTGCCTAGGAC
	AAGGGACCAA		GTTGCGCCAAG
	GGTGGAAATC		GGACCAAGGT
	AAACGGGCGG		GGAAATCAAA
	<b>CCGCAGAACA</b>		CGG (SEQ ID
	<b>AAAATCATC</b>		NO: 399)
	<b>TCAGAAGAGG</b>		
	<b>ATCTGAATTA</b>		
	<b>A</b> (SEQ ID		
	NO: 397)		
DMS7325	CDLPQTHSLGSRRT	TGCGACTTGCC	CDLPQTHSLG
(IFN $\alpha$ 2b-	LMLLAQMRRISLFS	ACAGACACAT	SRRTLMLLA
DOM7h-	CLKDRHDFGFPQE	AGTTTGGGATC	QMRRISLFS
11)	EFGNQFQKAETIPV	AAGAAGAACA	LKDRHDFGFP
	LHEMIQQIFNLFST	TTGATGTTATT	QEEFGNQFP
	KDSSAAWDELTD	AGCACAAATG	KAETIPVLHE
	KFYTELYQQLNDL	CGTAGAATTC	MIQQIFNLF
	EACVIQGVGTETP	TTTGTCTCTT	TKDSSAARD
	LMKEDSILAVRKY	GTCTAAAGGAC	ETLLDKFYTE
	FQRITLYLKEKYS	CGTCACGACT	LYQQLNDLE
	PCAWEVVRAEIMR	CGGATTCCTC	ACVIQGVGV
	SFSLSTNLQESLRS	AGGAAGAGTTT	TETPLMKEDS
	KETVAAPSDIQMT	GGAAACCAATT	ILAVRKYFQR
	QSPSSLSASVGDV	CCAAAAAGCA	ITLYLKEKKY
	TITCRASRPIGTTLS	GAAACTATTCC	SPCAWEVVR
	WYQQKPGKAPKLL	TGTCTGCACG	AEIMRSFSL
	IWFGSRLQSGVPSR	AAATGATCCAG	TNLQESLRSK
	FSGSGSGTDFTLTIS	CAAAATATCAA	ETVAAPSDIQ
	SLQPEDFATYCA	TTTGTCTCTA	MTQSPSSLSA
	QAGTHPTTFGQGT	CAAAGGACTC	SVGDRVTITC
	KVEIKR	ATCAGCCGCTT	RASRPIGTTL
	<b>AAAEQKLISEEDL</b>	GGGATGAAAC	SWYQQKPGK
<b>N*</b> (SEQ ID NO: 400)	TCTGTAGATA	APKLLIWFGS	AACTCTGTAG
	AATTCTACACT	RLQSGVPSRF	ATAAATTTCTAC
	GAACTATATCA	SGSGSGTDF	ACTGAACTATA
	ACAACCTGAAC	LTISLQPEDF	TCAACAACCTGA
	GATCTAGAGGC	ATYYCAQAG	ACGATCTAGA
	TTGCGTTATTC	THPTTFGQGT	GGCTTGCGTTA
	AGGGTGTAGG	KVEIKR (SEQ	TTCAGGGTGA
	AGTTACTGAAA	ID NO: 402)	GGAGTTACTGA
	CTCCCTAATG		AACTCCCTTAA
	AAAGAAGATT		TGAAAGAAGA
	CAATCTAGCC		TTCAATTTCTAG
	GTTAGAAAATA		CCGTTAGAAA
	CTTTCAGCGTA		ATACTTTCAGC
	TCACATTGTAT		GTATCACATTG
	TTAAAGGAAA		TATTTAAAGGA
	AGAAATACTCC		AAAGAAATAC
	CCATGTGCATG		TCCCATGTGC
	GGAGGTGGTTA		ATGGGAGGTG
	GAGCAGAAAT		GTTAGAGCAG
	TATGAGGTCTT		AAATTTATGAG
	TCTCTCTTCT		GTCTCTCTCTC
	ACGAATTTGCA		TTTCTACGAAT
	AGAACTTTGA		TTGCAAGAATC
	GATCTAAGGA		TTTGAGATCTA
	AACCGTCGCTG		AGGAAACCGT
	CTCCATCTGAC		CGCTGCTCCAT
	ATCCAGATGAC		CTGACATCCAG

TABLE 11-continued

Interferon alpha 2b-AlbudAb sequences with and without myc-tag (as amino acid- and nucleotide sequence) The Interferon alpha 2b is N-terminal to the AlbudAb in the following fusions.				
aa + myc	nt + myc	aa no tag	nt no tag	
	CCAGTCTCCAT		ATGACCCAGTC	
	CCTCCCTGTCT		TCCATCCTCCC	
	GCATCTGTAGG		TGTCTGCATCT	
	AGACCGTGTC		GTAGGAGACC	
	CCATCACTTGC		GTGTCACCATC	
	CGGGCAAGTC		ACTTGCCTGGC	
	GTCCTGTTGGG		AAGTCTCCGA	
	ACGACGTTAAG		TTGGGACGAC	
	TTGGTACCAGC		GTTAAGTTGGT	
	AGAAACCAGG		ACCAGCAGAA	
	GAAAGCCCCTA		ACCAGGGAAA	
	AGCTCCTGATC		GCCCTAAGCT	
	TGGTTGGTTC		CCTGATCTGGT	
	CCGGTTGCAAA		TTGGTTCCCGG	
	GTGGGGTCCCA		TTGCAAAGTGG	
	TCACGTTTCAG		GGTCCCATCAC	
	TGGCAGTGGAT		GTTTCAGTGGC	
	CTGGGACAGAT		AGTGGATCTGG	
	TTCACCTCAC		GACAGATTTCA	
	CATCAGCAGTC		CTCTCACCATC	
	TGCAACCTGAA		AGCAGTCTGCA	
	GATTTTGCTAC		ACCTGAAGATT	
	GTAATACTGTG		TTGCTACGTAC	
	CGCAGGCTGG		TACTGTGCGCA	
	GACGCATCCTA		GGCTGGGACG	
	CGACGTTCCGGC		CATCCTACGAC	
	CAAGGGACCA		GTTCCGCCAAG	
	AGGTGGAAAT		GGACCAAGGT	
	CAAACGGGCG		GGAAATCAAA	
	<b>GCCGCAGAAC</b>		CGG (SEQ ID	
	<b>AAAAACTCAT</b>		NO: 403)	
	<b>CTCAGAAGAG</b>			
	<b>GATCTGAATT</b>			
	<b>AA</b> (SEQ ID			
	NO: 401)			
DMS7326	CDLPQTHSLGSRRT	TGCGACTTGCC	CDLPQTHSLG	TGCGACTTGCC
(IFN $\alpha$ 2b-	LMLLAQMRRISLFS	ACAGACACAT	SRRLMMLLA	ACAGACACAT
DOM7h-	CLKDRHDFGFPQE	AGTTTGGGATC	QMRRISLFS	AGTTTGGGATC
11-12)	EFGNQFQKAETIPV	AAGAAGAACA	LKDRHDFGFP	AAGAAGAACA
	LHEMIQQIFNLFST	TTGATGTTATT	QEEFNGQFP	TTGATGTTATT
	KDSSAAWDELTD	AGCACAAATG	KAETIPVLHE	AGCACAAATG
	KFYTELYQQLNDL	CGTAGAATTC	MIQQIFNLF	CGTAGAATTC
	EACVIQGVGTETP	TTTGTCTCTT	TKDSSAARD	TTTGTCTCTT
	LMKEDSILAVRKY	GTCTAAAGGAC	ETLLDKFYTE	GTCTAAAGGAC
	FQRITLYLKEKKYS	CGTCACGACT	LYQQLNDLE	CGTCACGACT
	PCAWEVVRAEIMR	CGGATTCCTC	ACVIQGVGV	TCGGATTCCTC
	SFSLSTNLQESLRS	AGGAAGAGTTT	TETPLMKEDS	CAGGAAGAGT
	KETVAAPSDIQMT	GGAAACCAATT	ILAVRKYFQR	TTGAAACCA
	QSPSSLSASVGDV	CCAAAAAGCA	ITLYLKEKKY	ATTCCAAAA
	TITCRASRPIGTML	GAAACTATTC	SPCAWEVVR	GCAGAAACTA
	SWYQKPKGKAPKL	TGTCTGCACG	AEIMRSFSL	TTCTGTCTTG
	LILFGSRLQSGVPS	AAATGATCCAG	TNLQESLRSK	CACGAAATGA
	RFSGSGSSTDFTLT	CAAAATATCAA	ETVAAPSDIQ	TCCAGCAAATA
	ISSLQPEDFATYYC	TTTGTCTCTA	MTQSPSSLSA	TTCAATTTGTT
	AQAGTHPTTFGQG	CAAAGGACTC	SVGDRVTITC	TTCTACAAAGG
	TKVEIKR	ATCAGCCGCTT	RASRPIGTML	ACTCATCAGCC
	<b>AAAEQKLISEEDL</b>	GGGATGAAAC	SWYQKPKGK	GCTTGGGATGA
	<b>N*</b> (SEQ ID NO: 404)	TCTGTTAGATA	APKLLILFGS	AACTCTGTTAG
		AATTCTACACT	RLQSGVPSRF	ATAAATTTCTAC
		GAACTATATCA	SGSGSSTDF	ACTGAACTATA
		ACAACGAAAC	LTISSLQPEDF	TCAACAACGAA
		GATCTAGAGGC	ATYYCAQAG	ACGATCTAGA
		TTGCGTTATTC	THPTTFGQGT	GGCTTGGCTTA
		AGGGTGTAGG	KVEIKR (SEQ	TTCAGGGTGTG
		AGTTACTGAAA	ID NO: 406)	GGAGTTACTGA
		CTCCCTAATG		AACTCCCTTAA
		AAAGAAGATT		TGAAAGAAGA
		CAATTCTAGCC		TTCAATTTCTAG
		GTTAGAAAATA		CCGTTAGAAA
		CTTTCAGCGTA		ATACTTTCAGC
		TCACATTGTAT		GTATCACATTG
		TTAAAGGAAA		TATTTAAAGGA

TABLE 11-continued

Interferon alpha 2b-AlbudAb sequences with and without myc-tag (as amino acid- and nucleotide sequence) The Interferon alpha 2b is N-terminal to the AlbudAb in the following fusions.				
aa + myc	nt + myc	aa no tag	nt no tag	
	AGAAATACTCC		AAAGAAATAC	
	CCATGTGCATG		TCCCCATGTGC	
	GGAGGTGGTTA		ATGGGAGGTG	
	GAGCAGAAAT		GTAGAGCAG	
	TATGAGGTCT		AAATTATGAG	
	TCTCTTTTCT		GTCTTCTCTC	
	ACGAATTTGCA		TTTCTACGAAT	
	AGAATCTTTGA		TTGCAAGAATC	
	GATCTAAGGA		TTTGAGATCTA	
	AACCGTCGCTG		AGGAAACCGT	
	CTCCATCTGAC		CGCTGCTCCAT	
	ATCCAGATGAC		CTGACATCCAG	
	CCAGTCTCCAT		ATGACCCAGTC	
	CCTCCCTGTCT		TCCATCCTCCC	
	GCATCTGTAGG		TGTCTGCATCT	
	AGACCGTGTCA		GTAGGAGACC	
	CCATCACTTGC		GTGTCAACCATC	
	CGGGCAAGTC		ACTTCCGGGC	
	GTCCTGTTGGG		AAGTCGTCCGA	
	ACGATGTTAAG		TTGGGACGATG	
	TTGGTACCAGC		TTAAGTTGGTA	
	AGAAACCAGG		CCAGCAGAAA	
	GAAAGCCCTA		CCAGGGAAAG	
	AGCTCCTGATC		CCCCTAAGCTC	
	TTGTTGGTTC		CTGATCTTGT	
	CCGGTTGCAAA		TGGTCCCCTG	
	GTGGGGTCCCA		TGCAAAGTGG	
	TCACGTTTCAG		GGTCCCATCAC	
	TGGCAGTGGAT		GTTTCAGTGGC	
	CTGGGACAGAT		AGTGGATCTGG	
	TTCACTCTCAC		GACAGATTTCA	
	CATCAGCAGTC		CTCTCACCATC	
	TGCAACCTGAA		AGCAGTCTGCA	
	GATTTTGCTAC		ACCTGAAGATT	
	GTACTACTGTG		TTGCTACGTAC	
	CGCAGGCTGG		TACTGTGCGCA	
	GACGCATCCTA		GGCTGGGACG	
	CGACGTTCCGGC		CATCTACGAC	
	CAAGGGACCA		GTTCCGGCCAAG	
	AGGTGGAAAT		GGACCAAGGT	
	CAAACGGGCG		GGAAATCAA	
	<b>GCCGCAGAAC</b>		CGG (SEQ ID	
	<b>AAAAACTCAT</b>		NO: 407)	
	<b>CTCAGAAGAG</b>			
	<b>GATCTGAATT</b>			
	<b>AA</b> (SEQ ID			
	NO: 405			
DMS7327	CDLPQTHSLGSRRT	TGCGACTTGCC	CDLPQTHSLG	TGCGACTTGCC
(IFN $\alpha$ 2b-	LMLLAQMRRISLFS	ACAGACACAT	SRRTLMLLA	ACAGACACAT
DOM7h-	CLKDRHDFGFPQE	AGTTTGGGATC	QMRRISLFS	AGTTTGGGATC
11-15)	EFGNQFQKAETIPV	AAGAAGAACA	LKDRHDFGFP	AAGAAGAACA
	LHEMIQQIFNLFST	TTGATGTTATT	QEEFGNQFQ	TTGATGTTATT
	KDSSAAWDETLDD	AGCACAAATG	KAETIPVLHE	AGCACAAATG
	KFYTELYQQLNDL	CGTAGAATTC	MIQQIFNLFS	CGTAGAATTC
	EACVIQGVGVTEP	TTTGTCTCTT	TKDSSAARD	TTTGTCTCTT
	LMKEDSILAVRKY	GTCTAAAGGAC	ETLLDKFYTE	GTCTAAAGGAC
	FQRITLYLKEKKYS	CGTCACGACT	LYQQLNDLE	CGTCACGACT
	PCAWEVVRAEIMR	CGGATTCCTC	ACVIQGVGV	TCGGATTCCTC
	SFSLSTNLQESLRS	AGGAAGGTTT	TETPLMKEDS	CAGGAAGGT
	KETVAAPSDIQMT	GGAAACCAAT	ILAVRKYFQR	TTGAAACCA
	QSPSSLSASVGDV	CCAAAAAGCA	ITLYLKEKKY	ATTCCAAAA
	TITCRASRPIGTML	GAAACTATTC	SPCAWEVVR	GCAGAAACTA
	SWYQKPKKAPKL	TGTCTGCACG	AEIMRSFSL	TTCTGTCTGT
	LILAFSRLQSGVPS	AAATGATCCAG	TNLQESLSK	CACGAAATGA
	RFSGSGSSTDFTLT	CAAAATATCAA	ETVAAPSDIQ	TCCAGCAATA
	ISSLQPEDFATYYC	TTTGTCTCTA	MTQSPSSLSA	TTCAATTTGTT
	AQAGTHPTFFGQG	CAAAGGACTC	SVGDRVTITC	TTCTACAAAGG
	TKVEIKR	ATCAGCCGCTT	RASRPIGTML	ACTCATCAGCC
	<b>AAAEQKLISEEDL</b>	GGGATGAAAC	SWYQKPKGK	GCTGGGATGA
<b>N*</b> (SEQ ID NO: 408)	TCTGTTAGATA	APKLLILAFS		AACTCTGTTAG
	AATTCTACACT	RLQSGVPSRF		ATAAATTTCTAC
	GAACATATATCA	SGSGSGTDFT		ACTGAACTATA

TABLE 11-continued

Interferon alpha 2b-AlbudAb sequences with and without myc-tag (as amino acid- and nucleotide sequence) The Interferon alpha 2b is N-terminal to the AlbudAb in the following fusions.			
aa + myc	nt + myc	aa no tag	nt no tag
	ACAACTGAAC	LTISSLQPEDF	TCAACAACCTGA
	GATCTAGAGGC	ATYYCAQAG	ACGATCTAGA
	TTGCGTTATTC	THPTTFGQGT	GGCTTGCCTTA
	AGGGTGTAGG	KVEIKR (SEQ	TTCAGGGTGTGTA
	AGTTACTGAAA	ID NO: 410)	GGAGTTACTGA
	CTCCCCTAATG		AACTCCCCTAA
	AAAGAAGATT		TGAAAGAGAGA
	CAATCTAGCC		TTCAATCTTAG
	GTTAGAAAATA		CCGTTAGAAA
	CTTTCAGCGTA		ATACTTTCAGC
	TCACATTGTAT		GTATCACATTG
	TTAAGGAAA		TATTTAAGGA
	AGAAACTACC		AAAGAAATAC
	CCATGTGCATG		TCCCCATGTGC
	GGAGGTGGTTA		ATGGGAGGTG
	GAGCAGAAAT		GTAGAGCAG
	TATGAGGTCTT		AAATTATGAG
	TCTCTTTTCT		GTCCCTTCTCTC
	ACGAATTTGCA		TTTCTACGAAT
	AGAACTTTGA		TTGCAAGAATC
	GATCTAAGGA		TTTGATCTCA
	AACCGTCGCTG		AGGAAACCGT
	CTCCATCTGAC		CGCTGCTCCAT
	ATCCAGATGAC		CTGACATCCAG
	CCAGTCTCCAT		ATGACCCAGTC
	CCTCCCTGTCT		TCCATCCTCCC
	GCATCTGTAGG		TGTCTGCATCT
	AGACCGTGTCA		GTAGGAGACC
	CCATCACTTGC		GTGTCACCATC
	CGGGCAAGTC		ACTTGCCGGGC
	GTCCGATTGGG		AAGTCGTCCGA
	ACGATGTTAAG		TTGGGACGATG
	TTGGTACCAGC		TTAAGTTGGTA
	AGAAACCAGG		CCAGCAGAAA
	GAAAGCCCTA		CCAGGGAAAG
	AGCTCCTGATC		CCCCTAAGCTC
	CTTGCTTTTTC		CTGATCCTTGC
	CCGTTTGCAAA		TTTTTCCCCTT
	GTGGGTCCCA		TGCAAGTGG
	TCACGTTTCAG		GGTCCCATCAC
	TGGCAGTGGAT		GTTTCAGTGGC
	CTGGGACAGAT		AGTGGATCTGG
	TTCACTCTCAC		GACAGATTTCA
	CATCAGCAGTC		CTCTCACCATC
	TGCAACCTGAA		AGCAGTCTGCA
	GATTTTGCTAC		ACCTGAAGATT
	GTACTACTGCG		TTGCTACGTAC
	CGCAGGCTGG		TACTGCGCGCA
	GACGCATCCTA		GGCTGGGACG
	CGACGTTCCGGC		CATCCTACGAC
	CAAGGGACCA		GTTCGGCCAAG
	AGGTGGAAAT		GGACCAAGGT
	CAAACGGGCG		GGAAATCAAA
	<b>GCCGCAGAAC</b>		CGG (SEQ ID
	<b>AAAAACTCAT</b>		NO: 411)
	<b>CTCAGAGAG</b>		
	<b>GATCTGAATT</b>		
	<b>AA</b> (SEQ ID		
	NO: 409)		

The amino acid and nucleotide sequences highlighted in bold represents the cloning site and MYC tag.

\*represents the stop codon at the end of the gene.

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## Affinity Determination and Biophysical Characterisation:

To determine the binding affinity ( $K_D$ ) of the AlbuAb-IFN $\alpha$ 2b fusion proteins to each serum albumin; purified fusion proteins were analysed by BIAcore over albumin (immobilised by primary-amine coupling onto CM5 chips; BIAcore) using fusion protein concentrations from 5000 nM to 39 nM (5000 nM, 2500 nM, 1250 nM, 625 nM, 312 nM, 156 nM, 78 nM, 39 nM) in HBS-EP BIAcore buffer.

TABLE 12

Affinity to SA				
AlbuAb	Fusion	Affinity to		
		SA (nM)	Kd	Ka
Rat				
DOM7h-14	IFN $\alpha$ 2b	350	4.500E-02	1.28E+05
DOM7h-14-10	IFN $\alpha$ 2b	16	4.970E-03	5.90E+05
DOM 7h-14-18	IFN $\alpha$ 2b	780	2.127E-01	5.80E+05
DOM 7h-14-19	IFN $\alpha$ 2b	1900	1.206E-01	7.96E+04
DOM 7h-11	IFN $\alpha$ 2b	6000	7.500E-01	nd
DOM 7h-11-12	IFN $\alpha$ 2b	1700	3.100E-01	1.30E+05
DOM 7h-11-15	IFN $\alpha$ 2b	200	1.660E-02	1.50E+05
Cyno				
DOM 7h-14	IFN $\alpha$ 2b	60	1.32E-02	5.0E+05
DOM 7h-14-10	IFN $\alpha$ 2b	19	7.05E-03	4.50E+05
DOM 7h-14-18	IFN $\alpha$ 2b	no binding	no binding	no binding
DOM 7h-14-19	IFN $\alpha$ 2b	520	8.47E-02	2.73E+05
DOM 7h-11	IFN $\alpha$ 2b	3300	3.59E-01	1.20E+05
DOM 7h-11-12	IFN $\alpha$ 2b	630	3.45E-01	7.00E+05
DOM 7h-11-15	IFN $\alpha$ 2b	15	4.86E-03	3.60E+05
Mouse				
DOM 7h-14	IFN $\alpha$ 2b	240	3.21E-02	1.50E+06
DOM 7h-14-10	IFN $\alpha$ 2b	60	3.45E-02	6.86E+05
DOM 7h-14-18	IFN $\alpha$ 2b	180	1.50E-01	9.84E+05
DOM 7h-14-19	IFN $\alpha$ 2b	490	4.03E-02	1.19E+05
DOM 7h-11	IFN $\alpha$ 2b	6000	1.55E-01	nd
DOM 7h-11-12	IFN $\alpha$ 2b	150	9.49E-02	6.30E+05
DOM 7h-11-15	IFN $\alpha$ 2b	28	6.69E-03	2.80E+05
Human				
DOM 7h-14	IFN $\alpha$ 2b	244	2.21E-02	9.89E+04
DOM 7h-14-10	IFN $\alpha$ 2b	32	6.58E-03	3.48E+05
DOM 7h-14-18	IFN $\alpha$ 2b	470	2.75E-01	6.15E+05
DOM 7h-14-19	IFN $\alpha$ 2b	350	4.19E-02	1.55E+05
DOM 7h-11	IFN $\alpha$ 2b	670	2.02E-01	7.00E+05
DOM 7h-11-12	IFN $\alpha$ 2b	500	1.66E-01	3.90E+05
DOM 7h-11-15	IFN $\alpha$ 2b	10	1.87E-03	3.50E+05

When IFN $\alpha$ 2b is linked to the AlbuAb variants, in all cases the affinity of AlbuAb binding to serum albumin is reduced. DOM7h-14-10 and DOM7-11-15 retain improved

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binding affinity to serum albumin across species compared to parent. DOM7h-11-12 also shows improved binding affinity to serum albumin across species compared to parent.

TABLE 13

Biophysical Characterisation				
Biophysical Characterisation was carried out by SEC MALLS and DSC as described above for the single AlbuAbs.				
AlbuAb	Fusion	DMS number	Biophysical parameters	
			SEC MALLS	DSC Tm ( $^{\circ}$ C.)
DOM 7h-14	IFN $\alpha$ 2b	DMS7321	M/D	58-65
DOM 7h-14-10	IFN $\alpha$ 2b	DMS7322	M/D	55-65
DOM 7h-14-18	IFN $\alpha$ 2b	DMS7323	M/D	55-65
DOM 7h-14-19	IFN $\alpha$ 2b	DMS7324	M/D	59-66
DOM 7h-11	IFN $\alpha$ 2b	DMS7325	M/D	65.8-66.2
DOM 7h-11-12	IFN $\alpha$ 2b	DMS7326	M/D	67-67.3
DOM 7h-11-15	IFN $\alpha$ 2b	DMS7327	M/D	56.3-66.2

M/D indicates a monomer/dimer equilibrium as detected by SEC MALLS

We observed expression for all clones in Table 13 in the range of 17.5 to 54 mg/L in HEK293.

For IFN $\alpha$ 2b-DOM7h-14 and IFN $\alpha$ 2b-DOM7h-11 variants, favorable biophysical parameters and expression levels were maintained during affinity maturation.

PK Determination for AlbuAb-IFN $\alpha$ 2b Fusions

AlbuAbs IFN $\alpha$ 2b fusions DMS7321 (IFN $\alpha$ 2b-DOM7h-14) DMS7322 (IFN $\alpha$ 2b-DOM7h-14-10) DMS7323 (IFN $\alpha$ 2b-DOM7h-14-18), DMS7324 (IFN $\alpha$ 2b-DOM7h-14-19), DMS7325 (IFN $\alpha$ 2b-DOM7h-11), DMS7326 (IFN $\alpha$ 2b-DOM7h-11-12), DMS7327 (IFN $\alpha$ 2b-DOM7h-11-15) were expressed with the myc tag at 20-50 mg quantities in HEK293 cells and purified from culture supernatant using protein L affinity resin and eluted with 100 mM glycine pH2. The proteins were concentrated to greater than 1 mg/ml, buffer exchanged into Dulbecco's PBS and endotoxin depleted using Q spin columns (Vivascience).

For Rat PK, IFN-AlbuAbs were dosed as single i.v injections at 2.0 mg/kg using 3 rats per compound. Serum samples were taken at 0.16, 1, 4, 8, 24, 48, 72, 120, 168 hrs. Analysis of serum levels was by EASY ELISA according to manufacturers instructions (GE Healthcare, catalogue number RPN5960).

For Mouse PK, DMS7322 (IFN2b-DOM7h-14-10) DMS7325 (IFN2b-DOM7h-11), DMS7326 (IFN2b-DOM7h-11-12), DMS7327 (IFN2b-DOM7h-11-15) all with myc tags were dosed as single i.v injections at 2.0 mg/kg per dose group of 3 subjects and serum samples taken at 10 mins; 1 h; 8 h; 24 h; 48 h; 72 h; 96 h. Analysis of serum levels was by EASY ELISA according to manufacturers instructions (GE Healthcare, catalogue number RPN5960).

TABLE 14

Species	AlbudAb	Fusion	PK parameters				
			Albumin K <sub>D</sub> (nM)	AUC h × ug/ml	CL ml/h/kg	t <sub>1/2</sub> h	Vz ml/kg
Rat	7h-14	IFNα2b	350	832.1	2.4	27	94.5
	7h-14-10	IFNα2b	16	1380.7	1.5	35.8	75.2
	7h-14-18	IFNα2b	780	691.2	2.9	22.4	93.7
	7h-14-19	IFNα2b	1900	969.4	2.2	25	78.7
	7h-11	IFNα2b	6000	327.9	6.5	11	101.9
	7h-11-12	IFNα2b	1700	747.1	2.8	25.8	104.7
	7h-11-15	IFNα2b	200	1118.7	1.8	39.5	103.6
mouse	7h-14	IFNα2b	240	761.2	2.6	30.4	115.3
	7h-14-10	IFNα2b	60	750.5	2.7	30.9	118.6
	7h-11	IFNα2b	6000	493.9	4.0	8.8	51.2
	7h-11-12	IFNα2b	150	439.6	4.5	21.5	140.9
	7h-11-15	IFNα2b	28	971.8	2.1	33.6	99.6

Pharmacokinetic parameters derived from rat and mouse studies were fitted using a non-compartmental model. Key: AUC: Area under the curve from dosing time extrapolated to infinity; CL: clearance; t<sub>1/2</sub>: is the time during which the blood concentration is halved; Vz: volume of distribution based on the terminal phase.

IFNα2b—AlbudAbs were tested in rat and mouse. For all IFNα2b-DOM7h-11 variant fusion proteins in both rat and mouse, t<sub>1/2</sub> is improved compared to parent. The improvement in t<sub>1/2</sub> correlates with the improved in vitro K<sub>D</sub> to serum albumin. For IFNα2b-DOM7h-14-10 variants, the improvement in in vitro K<sub>D</sub> to serum albumin also correlated to an improvement in t<sub>1/2</sub> in rat.

All IFNα2b-AlbudAb fusion proteins exhibit a 5 to 10-fold decrease in the binding to RSA compared to the single AlbudAb. This effect is more pronounced (i.e. 10-fold) for the DOM7h-14 series than the DOM7h-11 series (only 5-fold decrease).

#### Example 8

#### Further AlbudAb Fusions with Proteins, Peptides and NCEs

Various AlbudAbs fused to other chemical entities namely domain antibodies (dAbs), peptides and NCEs were tested. The results are shown in table 15.

TABLE 15

Species	AlbudAb	Fusion	PK parameters				
			Albumin K <sub>D</sub> (nM)	AUC h × ug/ml	CL ml/h/kg	t <sub>1/2</sub> h	Vz ml/kg
Rat	DOM7h-14	Exendin-4	2400	18	57.1	11	901.9
	DOM7h-14-10	Exendin-4	19	43.6	23.1	22.1	740.3
	DOM7h-14-18	Exendin-4	16000	16.9	75.7	9.4	1002.5
	DOM7h-14-19	Exendin-4	17000	31.4	32.5	11.9	556.7
	DOM7h-11	Exendin-4	24000	6.1	168	7.1	1684.1
	DOM7h-11-12	Exendin-4	1400	24.2	59.9	13	1068.7
	DOM7h-11-15	Exendin-4	130	36.3	27.6	19.3	765.7
	DOM7h14-10	NCE- GGGGSC	62				
	DOM7h14-10	NCE- TVAAPSC	35				
	Human	DOM7h-14	NCE	204			
mouse	DOM7h-11	DOM1m- 21-23		234	10.7	4.7	72.5
	DOM7h-11-12	DOM1m- 21-23		755	3.3	18	86.2
	DOM7h-11-15	DOM1m- 21-23		1008	2.5	17.4	62.4

Key:

DOM1m-21-23 is an anti-TNFR1 dAb, Exendin-4 is a peptide (a GLP-1 agonist) of 39 amino acids length.

NCE, NCE-GGGGSC and NCE-TVAAPSC are described below.

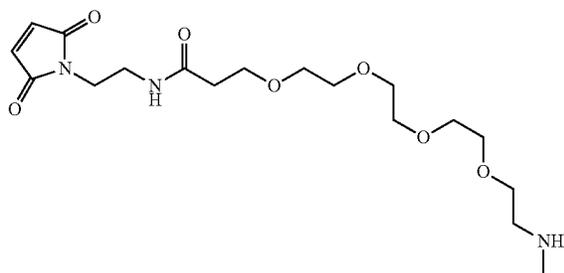
Previously we have described the use of genetic fusions with an albumin-binding dAb (AlbudAb) to extend the PK half-life of anti-TNFR1 dAbs in vivo (see, eg, WO04003019, WO2006038027, WO2008149148). Reference is made to the protocols in these PCT applications. In the table above, DOM1m-21-23 is an anti-mouse TNFR1 dAb.

To produce genetic fusions of exendin-4 or with DOM7h-14 (or other AlbudAb) which binds serum albumin, the exendin-4-linker-AlbudAb sequence was cloned into the pTT-5 vector (obtainable from CNRC, Canada). In each case the exendin-4 was at the 5' end of the construct and the dAb at the 3' end. The linker was a (G<sub>4</sub>S)<sub>3</sub> linker. Endotoxin-free DNA was prepared in *E. coli* using alkaline lysis (using the endotoxin-free plasmid Giga kit, obtainable from Qiagen CA) and used to transfect HEK293E cells (obtainable from CNRC, Canada). Transfection was into 250 ml/flask of HEK293E cells at 1.75×10<sup>6</sup> cells/ml using 333 ul of 293fectin (Invitrogen) and 250 ug of DNA per flask and expression was at 30° C. for 5 days. The supernatant was harvested by centrifugation and purification was by affinity purification on protein L. Protein was batch bound to the resin, packed on a column and washed with 10 column volumes of PBS. Protein was eluted with 50 ml of 0.1M glycine pH2 and neutralised with Tris pH8. Protein of the expected size was identified on an SDS-PAGE gel.

#### NCE Albudab Fusions:

A new chemical entity (NCE) AlbudAb fusion was tested. The NCE, a small molecule ADAMTS-4 inhibitor was synthesised with a PEG linker (PEG 4 linker (ie 4 PEG molecules before the maleimide) and a maleimide group for conjugation to the AlbudAb. Conjugation of the NCE to the AlbudAb is via an engineered cystine residue at amino acid position R108C, or following a 5 amino acid (GGGGSC (SEQ ID NO: 420)) or 6 amino acid (TVAAPSC (SEQ ID NO: 421)) spacer engineered at the end of the AlbudAb. Briefly, the AlbudAb was reduced with TCEP (Pierce, Catalogue Number 77720), desalted using a PD10 column (GE healthcare) into 25 mM Bis-Tris, 5 mM EDTA, 10% (v/v) glycerol pH6.5. A 5 fold molar excess of maleimide activated NCE was added in DMSO not to exceed 10% (V/V) final concentration. The reaction was incubated over night at room temperature and dialysed extensively into 20 mM Tris pH7.4

#### PEG Linker:



#### Sequences:

DOM7h-14-10 R108C:

(SEQ ID NO: 412)  
 DIQMTQSPSSLSASVGRVTTICTRASQWIGSQLSWYQQKPKAPKLLIMW  
 RSSLQSGVPSRFRSGSGSGTDFLTITSSLPEDFATYYCAQGLRHPKTFGQ  
 GTKVEIKC

Nucleotide:

(SEQ ID NO: 413)

5 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGA  
 CCGTGTCCACCATCACTTGCCGGGCAAGTCAGTGGATTGGGTCTCAGTTAT  
 CTTGGTACCAGCAGAAACCAGGGAAAGCCCCTAAGCTCCTGATCATGTGG  
 10 CGTTCTCGTTGCCAAGTGGGGTCCCATCACGTTTCAGTGGCAGTGGATC  
 TGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTG  
 15 CTACGTACTACTGTGCTCAGGGTTTGAGGCATCCTAAGACGTTTCGGCCAA  
 GGGACCAAGGTGGAATCAAATGC

See table 5 for the sequences of DOM7h-14-10/TVAAPSC (SEQ ID NO: 419) and DOM7h-14-10/GGGGSC (SEQ ID NO: 420) (ie, DOM7h-14-10/G4SC).

NCE-AlbudAbs DOM7h-14-10 GGGGSC (SEQ ID NO: 420) and DOM7h-14-10 TVAAPSC (SEQ ID NO: 419), exhibit a 5 to 10 fold decrease in in vitro affinity (K<sub>D</sub>) to RSA as determined by BIAcore when fused to the chemical entity. PK data are not available for these molecules yet.

dAb-Albudab fusion: the 2 DOM7h-11 AlbudAbs with the highest affinity to RSA experience a 2-fold decrease in affinity to RSA as on BIAcore when fused to a therapeutic domain antibody (DOM1m-21-23) compared to the unfused AlbudAb. The DOM7h-11 clone shows a micromolar K<sub>D</sub> when fused (2.8 uM) as well as when unfused (~5 uM).

Exendin 4-AlbudAb fusion: the effect of fusing the AlbudAbs to a peptide on the binding ability to RSA is about 10-fold, apart from DOM7h-14-10, which only shows a 4-fold decrease in binding. The effect, however, is more pronounced for the DOM7h-14 series (except DOM7h-14-10) than it appears to be for the DOM7h-11 series.

For all the above data, the T<sub>1/2</sub> of the fusion increased with improved affinity to the species' SA.

We generally classify Albudab-therapeutics as being therapeutically amenable (for treatment and/or prophylaxis of diseases, conditions or indications) when the AlbudAb-drug fusions show an affinity range (K<sub>D</sub>) of from 0.1 nM to 10 nM for serum albumin binding.

We define the therapeutic ranges of AlbudAbs and AlbudAb fusions (Protein-AlbudAbs for example IFNa2b-DOM7h-14-10; Peptide-AlbudAbs for example Exendin-4-DOM7h-14-10; dAb-AlbudAbs for example DOM1m21-23-DOM7h11-15; NCE-AlbudAb for example ADAMTS-4-DOM7h-14-10) as follows: Affinity (K<sub>D</sub>) ranges that are useful for therapy of chronic or acute conditions, diseases or indications are shown. Also shown are affinity ranges marked as "intermediate". AlbudAbs and fusions in this range have utility for chronic or acute diseases, conditions or indications. In this way, the affinity of the AlbudAb or fusion for serum albumin can be tailored or chosen according to the disease, condition or indication to be addressed. As described above, the invention provides AlbudAbs with affinities that allow for each AlbudAb to be categorised as "high affinity", "medium affinity" or "low affinity", thus enabling the skilled person to select the appropriate AlbudAb of the invention according to the therapy at hand. See FIG. 2.

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Example 9

DOM7h-11-15<sup>S12P</sup> Sequences

Amino Acid Sequence of DOM7h-11-15<sup>S12P</sup>

(SEQ ID NO: 414)  
 DIQMTQSPSSLFASVGRVTITCRASRPITMLSWYQQKPGKAPKLLILA  
 FSRLQSGVPSRFRSGSGSDFTLTISSLPEDFATYYCAQAGTHPTTFGQ  
 10  
 GTKVEIKR

An aspect of the invention provides a nucleic acid comprising the nucleotide sequence of DOM7h-11-15<sup>S12P</sup> or a nucleotide sequence that is at least 80% identical to said selected sequence. DOM7h-11-15<sup>S12P</sup> was produced using the following nucleic acid sequence (the underlined C denotes the change (versus the nucleic acid encoding DOM7h-11-15) leading to a proline at position 12):—

(SEQ ID NO: 415)  
 GACATCCAGATGACCCAGTCTCCATCCTCCCTGCTGCATCTGTAGGAGA  
 CCGTGTCCACCATCACTTGCCGGGCAAGTCGTCGATTGGGACGATGTTAA  
 GTTGGTACCAGCAGAAACCAGGGAAGCCCCCTAAGCTCCTGATCCTTGCT  
 25  
 TTTTCCCGTTTGCAAAGTGGGTCCCATCAGTTTCAGTGGCAGTGGATC

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-continued

TGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGATTTTG  
 CTACGTACTACTGCGCGCAGGCTGGGACGCATCCTACGACGTTTCGGCCA  
 5 AGGGACCAAGGTGGAAATCAAACGG

DOM7h-11-15<sup>S12P</sup> was constructed by using DOM7h-11-15 as a template in a PCR where a primer was used to introduce the S12P mutation. The primer sequence is:—

(SEQ ID NO: 416)  
 GCAACAGCGTCGACGGACATCCAGATGACCCAGTCTCCATCCTCCCTGCC  
 TGCATCTGTAGG.

15 An alternative aspect of the invention provides a nucleic acid comprising the nucleotide sequence of SEQ ID NO: 415 or a nucleotide sequence that is at least 80% identical to said selected sequence. In one embodiment, DOM7h-11-15<sup>S12P</sup> is encoded by, and expressed from, a vector that contains a  
 20 linker region and a C-terminal sequence encoding a protein or peptide drug or a single variable domain or other antibody fragment to make the in-line protein fusion product. The linker, in one embodiment, comprises the amino acid  
 25 sequence TVA, eg, TVAAPS (SEQ ID NO: 421). Other aspects of the invention are a vector comprising the nucleic acid; and an isolated host cell comprising the vector. The invention also provides a method of treating or preventing a disease or disorder in a patient, comprising administering at least one dose of DOM7h-11-15<sup>S12P</sup> to said patient.

SEQUENCE LISTING

<160> NUMBER OF SEQ ID NOS: 422

<210> SEQ ID NO 1  
 <211> LENGTH: 108  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 1

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Trp Ile Gly Ser Gln  
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Met Trp Arg Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Gly Leu Arg His Pro Lys  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg  
 100 105

<210> SEQ ID NO 2  
 <211> LENGTH: 108  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

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&lt;400&gt; SEQUENCE: 2

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1           5           10           15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Trp Ile Gly Ser Gln
 20           25           30
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35           40           45
Met Trp Arg Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50           55           60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65           70           75           80
Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Gly Leu Met Lys Pro Met
 85           90           95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100           105

```

&lt;210&gt; SEQ ID NO 3

&lt;211&gt; LENGTH: 108

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 3

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1           5           10           15
Asp Arg Val Thr Ile Ser Cys Arg Ala Ser Gln Trp Ile Gly Ser Gln
 20           25           30
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Glu Ala Pro Lys Leu Leu Ile
 35           40           45
Met Trp Arg Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50           55           60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65           70           75           80
Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Gly Ala Ala Leu Pro Arg
 85           90           95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 100           105

```

&lt;210&gt; SEQ ID NO 4

&lt;211&gt; LENGTH: 108

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 4

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Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1           5           10           15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Trp Ile Gly Ser Gln
 20           25           30
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
 35           40           45
Met Trp Arg Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
 50           55           60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65           70           75           80

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-continued

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Gly Ala Ala Leu Pro Lys  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg  
 100 105

<210> SEQ ID NO 5  
 <211> LENGTH: 108  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 5

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
 1 5 10 15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Trp Ile Gly Ser Gln  
 20 25 30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
 35 40 45

Met Trp Arg Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
 50 55 60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro  
 65 70 75 80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Gly Phe Lys Lys Pro Arg  
 85 90 95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg  
 100 105

<210> SEQ ID NO 6  
 <211> LENGTH: 324  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

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atcaacttgcc gggcaagtca gtggattggg tctcagttat cttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcatgtgg cgttcctcgt tgcaaagtgg ggtccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

gaagattttg ctacgtacta ctgtgctcag ggtttgaggc atcctaagac gttcggccaa 300

gggaccaagg tggaaatcaa acgg 324

<210> SEQ ID NO 7  
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 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

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atcaacttgcc gggcaagtca gtggattggg tctcagttat cttggtacca gcagaaacca 120

gggaaagccc ctaagctcct gatcatgtgg cgttcctcgt tgcaaagtgg ggtccatca 180

cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240

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 gggaccaagg tggaaatcaa acgg 324

<210> SEQ ID NO 8  
 <211> LENGTH: 324  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

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 atctcttgcc gggcaagtca gtggattggg tctcagttat cttggtacca gcagaaacca 120  
 ggggaagccc ctaagctcct gatcatgtgg cgttcctcgt tgcaaagtgg ggtcccatca 180  
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
 gaagattttg ctacgtacta ctgtgctcag ggtgcggcgt tgcctaggac gttcggccaa 300  
 gggaccaagg tggaaatcaa acgg 324

<210> SEQ ID NO 9  
 <211> LENGTH: 324  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

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 atcacttgcc gggcaagtca gtggattggg tctcagttat cttggtacca gcagaaacca 120  
 gggaaagccc ctaagctcct gatcatgtgg cgttcctcgt tgcaaagtgg ggtcccatca 180  
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
 gaagattttg ctacatacta ctgtgctcag ggtgcggcgt tgcctaagac gttcggccaa 300  
 gggaccaagg tggaaatcaa acgg 324

<210> SEQ ID NO 10  
 <211> LENGTH: 324  
 <212> TYPE: DNA  
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 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 10

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 atcacttgcc gggcaagtca gtggattggg tctcagttat cttggtacca gcagaaacca 120  
 gggaaagccc ctaagctcct gatcatgtgg cgttcctcgt tgcaaagtgg ggtcccatca 180  
 cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240  
 gaagattttg ctacgtacta ctgtgctcag ggttttaaga agcctcggac gttcggccaa 300  
 gggaccaagg tggaaatcaa acgg 324

<210> SEQ ID NO 11  
 <211> LENGTH: 120  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 11

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

-continued

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1	5	10	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gln Tyr	20	25	30
Arg Met His Trp Val Arg Gln Ala Pro Gly Lys Ser Leu Glu Trp Val	35	40	45
Ser Ser Ile Asp Thr Arg Gly Ser Ser Thr Tyr Tyr Ala Asp Pro Val	50	55	60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	65	70	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	85	90	95
Ala Lys Ala Val Thr Met Phe Ser Pro Phe Phe Asp Tyr Trp Gly Gln	100	105	110
Gly Thr Leu Val Thr Val Ser Ser	115	120	

<210> SEQ ID NO 12  
 <211> LENGTH: 123  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 12

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	1	5	10	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ala Asp Tyr	20	25	30	
Gly Met Arg Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	35	40	45	
Ser Ser Ile Thr Arg Thr Gly Arg Val Thr Tyr Tyr Ala Asp Ser Val	50	55	60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	65	70	75	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	85	90	95	
Ala Lys Trp Arg Asn Arg His Gly Glu Tyr Leu Ala Asp Phe Asp Tyr	100	105	110	
Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ser	115	120		

<210> SEQ ID NO 13  
 <211> LENGTH: 120  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 13

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	1	5	10	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Met Arg Tyr	20	25	30	
Arg Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	35	40	45	
Ser Ser Ile Asp Ser Asn Gly Ser Ser Thr Tyr Tyr Ala Asp Ser Val	50	55	60	

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Asp Arg Thr Glu Arg Ser Pro Val Phe Asp Tyr Trp Gly Gln  
100 105 110

Gly Thr Leu Val Thr Val Ser Ser  
115 120

<210> SEQ ID NO 14  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 14

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Asp Tyr  
20 25 30

Glu Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Ser Ile Ser Glu Ser Gly Thr Thr Thr Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Arg Arg Phe Ser Ala Ser Thr Phe Asp Tyr Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 15  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 15

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gln Ile Ser Asn Thr Gly Gly His Thr Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Tyr Thr Gly His Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

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<210> SEQ ID NO 16  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 16

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr
 20           25           30
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35           40           45
Ser Gln Ile Ser Asn Thr Gly Gly His Thr Tyr Tyr Ala Asp Ser Val
 50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65           70           75           80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85           90           95
Ala Lys Tyr Thr Gly Arg Trp Glu Pro Tyr Asp Tyr Trp Gly Gln Gly
 100          105          110
Thr Leu Val Thr Val Ser Ser
 115

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<210> SEQ ID NO 17  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 17

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr
 20           25           30
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35           40           45
Ser Gln Ile Ser Asn Thr Gly Gly His Thr Tyr Tyr Ala Asp Ser Val
 50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65           70           75           80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85           90           95
Ala Lys Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly
 100          105          110
Thr Leu Val Thr Val Ser Ser
 115

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<210> SEQ ID NO 18  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 18

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Gly Gly His Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 19  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 19

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Gly Gly His Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 20  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 20

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Gly Gly His Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Met Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 21  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 21

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Lys Tyr  
20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Asp Leu Glu Trp Val  
35 40 45

Ser Gln Ile Ser Asn Thr Gly Gly His Thr Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 22  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 22

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gln Ile Ser Asn Thr Gly Gly His Thr Tyr Tyr Ala Asp Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Lys Tyr Thr Gly Arg Trp Glu Pro Phe Asp His Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser

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<210> SEQ ID NO 23  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 23

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Gly Asp His Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Lys Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 24  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 24

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Lys Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 25  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 25

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 26  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 26

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Gly Asp His Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 27  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 27

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val

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50                    55                    60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65                                    70                                    75                                    80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                                          85                                    90                                    95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
                                          100                                    105                                    110

Thr Leu Val Thr Val Ser Ser  
                                          115

<210> SEQ ID NO 28  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 28

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1                                    5                                    10                                    15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
                                          20                                    25                                    30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Val  
                                          35                                    40                                    45

Ser Gln Ile Ser Asn Thr Gly Asp His Thr Tyr Tyr Ala Asp Ser Val  
50                                    55                                    60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65                                    70                                    75                                    80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                                          85                                    90                                    95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
                                          100                                    105                                    110

Thr Leu Val Thr Val Ser Ser  
                                          115

<210> SEQ ID NO 29  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 29

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1                                    5                                    10                                    15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Lys Tyr  
                                          20                                    25                                    30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Asp Leu Glu Trp Val  
                                          35                                    40                                    45

Ser Gln Ile Ser Asn Thr Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val  
50                                    55                                    60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65                                    70                                    75                                    80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                                          85                                    90                                    95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
                                          100                                    105                                    110

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Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 30  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 30

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Lys Tyr  
20 25 30  
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Asp Leu Glu Trp Val  
35 40 45  
Ser Gln Ile Ser Asn Thr Gly Asp His Thr Tyr Tyr Ala Asp Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
100 105 110  
Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 31  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 31

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
20 25 30  
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Ser Gln Ile Ser Asn Thr Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly  
100 105 110  
Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 32  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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&lt;400&gt; SEQUENCE: 32

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

&lt;210&gt; SEQ ID NO 33

&lt;211&gt; LENGTH: 119

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 33

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Lys Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

&lt;210&gt; SEQ ID NO 34

&lt;211&gt; LENGTH: 119

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 34

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

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Ser Gln Ile Ser Asn Thr Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Ile Tyr Thr Gly Arg Trp Val Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 35  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 35

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gln Ile Ser Asn Thr Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Ile Tyr Thr Gly Arg Trp Arg Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 36  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 36

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gln Ile Ala Asn Thr Gly Asp Arg Arg Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ala Tyr Tyr Cys  
 85 90 95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
 100 105 110

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Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 37  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 37

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
20 25 30  
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Ser Gln Ile Ser Asn Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asn Tyr Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 38  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 38

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
20 25 30  
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Ser Gln Ile Ser Asn Thr Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 39  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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&lt;400&gt; SEQUENCE: 39

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Ser Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Val Pro Phe Asp Asn Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

&lt;210&gt; SEQ ID NO 40

&lt;211&gt; LENGTH: 119

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 40

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ile Thr Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Gln Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

&lt;210&gt; SEQ ID NO 41

&lt;211&gt; LENGTH: 119

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 41

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Gly Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

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Ser Gln Ile Ser Asn Thr Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 42  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 42

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Lys Tyr  
 20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gln Ile Ser Asn Thr Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 43  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 43

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gln Ile Ser Asp Thr Gly Asp Arg Arg Tyr Tyr Asp Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly

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100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 44  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 44

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
20 25 30  
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Ser Gln Ile Ser Asn Thr Gly Asp Arg Arg Tyr Tyr Ala Asp Ala Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
100 105 110  
Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 45  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 45

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
20 25 30  
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Ser Gln Ile Ser Asn Thr Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Lys Tyr Trp Gly Gln Gly  
100 105 110  
Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 46  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:

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<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 46

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Gly Glu Arg Arg Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Pro Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 47

<211> LENGTH: 119

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 47

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Asn Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Glu Pro Tyr Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Thr Ser  
 115

<210> SEQ ID NO 48

<211> LENGTH: 119

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 48

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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      35              40              45
Ser  Gln Ile Ala Asn Thr Gly Asp Arg Arg Tyr Tyr Ala Asp Ser Val
   50              55              60
Lys  Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
   65              70              75              80
Leu  Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
           85              90              95
Ala  Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly
           100             105             110
Thr  Leu Val Thr Val Ser Ser
           115

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<210> SEQ ID NO 49
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 49

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
  1              5              10             15
Ser  Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr
           20              25              30
Ser  Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
           35              40              45
Ser  Gln Ile Ala Asn Thr Gly Asp Arg Arg Tyr Tyr Ala Asp Ser Val
           50              55              60
Lys  Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
           65              70              75              80
Leu  Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
           85              90              95
Ala  Ile Tyr Thr Gly Arg Trp Lys Pro Phe Glu Tyr Trp Gly Gln Gly
           100             105             110
Thr  Leu Val Thr Val Ser Ser
           115

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<210> SEQ ID NO 50
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 50

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
  1              5              10             15
Ser  Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr
           20              25              30
Ser  Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
           35              40              45
Ser  Gln Ile Ala Asn Thr Gly Asp Arg Arg Tyr Tyr Ala Asp Ser Val
           50              55              60
Lys  Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
           65              70              75              80
Leu  Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
           85              90              95

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Ala Ile Tyr Thr Gly Arg Trp Val Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 51  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 51

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gln Ile Ala Asn Thr Gly Asp Arg Arg Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Ile Tyr Thr Gly Arg Trp Arg Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 52  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 52

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gln Ile Ala Asn Thr Gly Asp Arg Arg Tyr Tyr Ala Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 53  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 53

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Val Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 54  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 54

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Lys Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 55  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 55

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30



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Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 58  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 58

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gln Ile Ser Asp Thr Gly Asp Arg Arg Tyr Tyr Asp Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 59  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 59

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gln Ile Ser Asp Thr Gly Asp Arg Arg Tyr Tyr Asp Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Ile Tyr Thr Gly Arg Trp Lys Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 60  
 <211> LENGTH: 119  
 <212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 60

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asp Thr Gly Asp Arg Arg Tyr Tyr Asp Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Val Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 61  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 61

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asp Thr Gly Asp Arg Arg Tyr Tyr Asp Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Arg Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 62  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 62

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30

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Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
                   35                                  40                                  45

Ser Gln Ile Ser Asp Thr Gly Asp Arg Arg Tyr Tyr Asp Asp Ser Val  
           50                                  55                                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
   65                                  70                                  75                                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                   85                                  90                                  95

Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly  
                   100                                  105                                  110

Thr Leu Val Thr Val Ser Ser  
           115

<210> SEQ ID NO 63  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 63

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
   1                  5                                  10                                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
           20                                  25                                  30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
                   35                                  40                                  45

Ser Gln Ile Ser Asn Thr Gly Asp Arg Arg Tyr Tyr Ala Asp Ala Val  
   50                                  55                                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
   65                                  70                                  75                                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                   85                                  90                                  95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly  
                   100                                  105                                  110

Thr Leu Val Thr Val Ser Ser  
           115

<210> SEQ ID NO 64  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 64

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
   1                  5                                  10                                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
           20                                  25                                  30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
                   35                                  40                                  45

Ser Gln Ile Ser Asn Thr Gly Asp Arg Arg Tyr Tyr Ala Asp Ala Val  
   50                                  55                                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
   65                                  70                                  75                                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

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	85	90	95
Ala Ile Tyr Thr Gly Arg Trp Lys Pro Phe Glu Tyr Trp Gly Gln Gly	100	105	110
Thr Leu Val Thr Val Ser Ser	115		

<210> SEQ ID NO 65  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 65

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	5	10	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr	20	25	30
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	35	40	45
Ser Gln Ile Ser Asn Thr Gly Asp Arg Arg Tyr Tyr Ala Asp Ala Val	50	55	60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	65	70	75
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	85	90	95
Ala Ile Tyr Thr Gly Arg Trp Val Pro Phe Glu Tyr Trp Gly Gln Gly	100	105	110
Thr Leu Val Thr Val Ser Ser	115		

<210> SEQ ID NO 66  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 66

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	5	10	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr	20	25	30
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	35	40	45
Ser Gln Ile Ser Asn Thr Gly Asp Arg Arg Tyr Tyr Ala Asp Ala Val	50	55	60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	65	70	75
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	85	90	95
Ala Ile Tyr Thr Gly Arg Trp Arg Pro Phe Glu Tyr Trp Gly Gln Gly	100	105	110
Thr Leu Val Thr Val Ser Ser	115		

<210> SEQ ID NO 67  
 <211> LENGTH: 119

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<212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 67

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Gly Asp Arg Arg Tyr Tyr Ala Asp Ala Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 68  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 68

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Leu Lys Phe  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ala Asn Thr Gly Asp Arg Arg Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 69  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 69

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Leu Lys Tyr

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	20	25	30	
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	35	40	45	
Ser Gln Ile Ser Asn Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val	50	55	60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	65	70	75	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	85	90		95
Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly	100	105	110	
Thr Leu Val Thr Val Ser Ser	115			

<210> SEQ ID NO 70  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 70

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	1	5	10	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Lys Tyr	20	25	30	
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	35	40	45	
Ser Gln Ile Ser Asp Thr Gly Asp Arg Arg Tyr Tyr Asp Asp Ser Val	50	55	60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	65	70	75	80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	85	90		95
Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly	100	105	110	
Thr Leu Val Thr Val Ser Ser	115			

<210> SEQ ID NO 71  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 71

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	1	5	10	15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Leu Lys Tyr	20	25	30	
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	35	40	45	
Ser Gln Ile Ser Asp Thr Gly Asp Arg Arg Tyr Tyr Asp Asp Ser Val	50	55	60	
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	65	70	75	80

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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                                   85                                  90                                  95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly  
                                   100                                  105                                  110

Thr Leu Val Thr Val Ser Ser  
                                   115

<210> SEQ ID NO 72  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 72

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
   1                                  5                                  10                                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
                                   20                                  25                                  30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
                                   35                                  40                                  45

Ser Gln Ile Ala Asn Thr Gly Asp Arg Arg Tyr Tyr Ala Asp Ser Val  
   50                                  55                                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
   65                                  70                                  75                                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ala Tyr Tyr Cys  
                                   85                                  90                                  95

Ala Ile Tyr Thr Gly Arg Trp Pro Asp Phe Asp Tyr Trp Gly Gln Gly  
                                   100                                  105                                  110

Thr Leu Val Thr Val Ser Ser  
                                   115

<210> SEQ ID NO 73  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 73

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
   1                                  5                                  10                                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
                                   20                                  25                                  30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
                                   35                                  40                                  45

Ser Gln Ile Ala Asn Thr Gly Asp Arg Arg Tyr Tyr Ala Asp Ser Val  
   50                                  55                                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
   65                                  70                                  75                                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Ala Tyr Tyr Cys  
                                   85                                  90                                  95

Ala Ile Tyr Thr Gly Arg Trp Pro Asp Phe Glu Tyr Trp Gly Gln Gly  
                                   100                                  105                                  110

Thr Leu Val Thr Val Ser Ser  
                                   115

<210> SEQ ID NO 74

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<211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 74

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Pro Asp Phe Asp Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 75  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 75

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Pro Asp Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 76  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 76

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

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Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
                   20                                          25                                          30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
                   35                                          40                                          45

Ser Gln Ile Ser Asp Thr Gly Asp Arg Arg Tyr Tyr Asp Asp Ser Val  
                   50                                          55                                          60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
                   65                                          70                                          75                                          80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                   85                                          90                                          95

Ala Ile Tyr Thr Gly Arg Trp Pro Asp Phe Asp Tyr Trp Gly Gln Gly  
                   100                                          105                                          110

Thr Leu Val Thr Val Ser Ser  
                   115

<210> SEQ ID NO 77  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 77

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
   1                  5                                          10                                          15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
                   20                                          25                                          30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
                   35                                          40                                          45

Ser Gln Ile Ser Asp Thr Gly Asp Arg Arg Tyr Tyr Asp Asp Ser Val  
                   50                                          55                                          60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
                   65                                          70                                          75                                          80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                   85                                          90                                          95

Ala Ile Tyr Thr Gly Arg Trp Pro Asp Phe Glu Tyr Trp Gly Gln Gly  
                   100                                          105                                          110

Thr Leu Val Thr Val Ser Ser  
                   115

<210> SEQ ID NO 78  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 78

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
   1                  5                                          10                                          15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
                   20                                          25                                          30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Val  
                   35                                          40                                          45

Ser Gln Ile Ser Ala Trp Gly Asp Arg Thr Tyr Tyr Ala Asp Ser Val  
                   50                                          55                                          60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
                   65                                          70                                          75                                          80

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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                   85                                  90                                  95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
                   100                                  105                                  110

Thr Leu Val Thr Val Ser Ser  
           115

<210> SEQ ID NO 79  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 79

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1                  5                                  10                                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
           20                                  25                                  30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Val  
           35                                  40                                  45

Ser Gln Ile Ser Asp Gly Gly Gln Arg Thr Tyr Tyr Ala Asp Ser Val  
           50                                  55                                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
           65                                  70                                  75                                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                   85                                  90                                  95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
                   100                                  105                                  110

Thr Leu Val Thr Val Ser Ser  
           115

<210> SEQ ID NO 80  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 80

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1                  5                                  10                                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
           20                                  25                                  30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Val  
           35                                  40                                  45

Ser Gln Ile Ser Asp Ser Gly Tyr Arg Thr Tyr Tyr Ala Asp Ser Val  
           50                                  55                                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
           65                                  70                                  75                                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                   85                                  90                                  95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
                   100                                  105                                  110

Thr Leu Val Thr Val Ser Ser  
           115

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<210> SEQ ID NO 81  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 81

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asp Gly Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 82  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 82

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asp Lys Gly Thr Arg Thr Tyr Tyr Ala Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Asp Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 83  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 83

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15



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65              70              75              80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
              85              90              95
Ala Ile Tyr Thr Gly Arg Trp Val Pro Phe Glu Tyr Trp Gly Gln Gly
              100              105              110
Thr Leu Val Thr Val Ser Ser
              115

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<210> SEQ ID NO 86
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 86

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1              5              10              15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr
              20              25              30
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Pro Glu Trp Val
              35              40              45
Ser Gln Ile Ser Asn Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val
              50              55              60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65              70              75              80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
              85              90              95
Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly
              100              105              110
Thr Leu Val Thr Val Ser Ser
              115

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<210> SEQ ID NO 87
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 87

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1              5              10              15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr
              20              25              30
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
              35              40              45
Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val
              50              55              60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65              70              75              80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
              85              90              95
Ala Ile Tyr Thr Gly Arg Trp Val Pro Phe Glu Tyr Trp Gly Gln Gly
              100              105              110
Thr Leu Val Thr Val Ser Ser
              115

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<210> SEQ ID NO 88  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 88

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 89  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 89

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Asp Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Arg Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 90  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 90

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly

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1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr
    20           25           30
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
    35           40           45
Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Thr His Ser Val
    50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
    65           70           75           80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
    85           90           95
Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly
    100          105          110
Thr Leu Val Thr Val Ser Ser
    115

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<210> SEQ ID NO 91
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 91

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr
    20           25           30
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
    35           40           45
Ser Gln Ile Ser Asn Thr Ala Asp Arg Arg Tyr Tyr Ala His Ser Val
    50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
    65           70           75           80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
    85           90           95
Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly
    100          105          110
Thr Leu Val Thr Val Ser Ser
    115

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<210> SEQ ID NO 92
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 92

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr
    20           25           30
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
    35           40           45
Ser Gln Ile Leu Asn Thr Ala Asp Arg Thr Tyr Tyr Asp His Ser Val
    50           55           60

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 93  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 93

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gln Ile Ser Asn Thr Ala Asp Arg Thr Tyr Tyr Asp His Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 94  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 94

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gln Ile Ser Asp Thr Ala Asp Arg Arg Tyr Tyr Ala His Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

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<210> SEQ ID NO 95  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 95

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr
 20           25           30
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35           40           45
Ser Gln Ile Ser Asp Thr Ala Asp Arg Arg Tyr Tyr Asp His Ser Val
 50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65           70           75           80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85           90           95
Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly
 100          105          110
Thr Leu Val Thr Val Ser Ser
 115

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<210> SEQ ID NO 96  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 96

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr
 20           25           30
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35           40           45
Ser Gln Ile Ser Asn Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val
 50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65           70           75           80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85           90           95
Ala Val Tyr Thr Gly Arg Trp Val Ser Phe Glu Tyr Trp Gly Gln Gly
 100          105          110
Thr Leu Val Thr Val Ser Ser
 115

```

<210> SEQ ID NO 97  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 97

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Leu Tyr Thr Gly Arg Trp Val Ser Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 98  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 98

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Val Tyr Thr Gly Arg Trp Val Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 99  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 99

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val  
 50 55 60

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Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Leu Tyr Thr Gly Arg Trp Val Pro Phe Glu Tyr Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 100  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 100

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gln Ile Ala Asn Thr Ala Asp Arg Arg Tyr Tyr Ala His Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 101  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 101

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gln Ile Ser Asn Thr Ala Asp Arg Arg Tyr Tyr Ala Asp Ala Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser

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115

<210> SEQ ID NO 102  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 102

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Gly Asp Arg Arg Tyr Tyr Ala His Ala Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 103  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 103

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ala Asn Thr Ala Asp Arg Arg Tyr Tyr Ala Asp Ala Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 104  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 104

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ala Asn Thr Gly Asp Arg Arg Tyr Tyr Ala His Ala Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 105  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.  
 <400> SEQUENCE: 105

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asn Thr Ala Asp Arg Arg Tyr Tyr Ala His Ala Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 106  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.  
 <400> SEQUENCE: 106

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ala Asn Thr Ala Asp Arg Arg Tyr Tyr Ala His Ala Val

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50          55          60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65          70          75          80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85          90          95
Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly
100         105         110
Thr Leu Val Thr Val Ser Ser
115

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<210> SEQ ID NO 107
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 107

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr
20         25         30
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35         40         45
Ser Gln Ile Val Asn Thr Gly Asp Arg Arg Tyr Tyr Ala Asp Ala Val
50         55         60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65          70          75          80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85          90          95
Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly
100         105         110
Thr Leu Val Thr Val Ser Ser
115

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<210> SEQ ID NO 108
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 108

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
1          5          10          15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr
20         25         30
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35         40         45
Ser Gln Ile Ala Asn Thr Gly Asp Arg Arg Tyr Tyr Ala Asp Ala Val
50         55         60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65          70          75          80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
85          90          95
Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly
100         105         110

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Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 109  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 109

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
20 25 30  
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Asp His Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly  
100 105 110  
Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 110  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 110

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
20 25 30  
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Asp His Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Ile Tyr Thr Gly Arg Trp Arg Pro Phe Glu Tyr Trp Gly Gln Gly  
100 105 110  
Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 111  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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&lt;400&gt; SEQUENCE: 111

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Asp His Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

&lt;210&gt; SEQ ID NO 112

&lt;211&gt; LENGTH: 119

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 112

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Ser His Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Val Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

&lt;210&gt; SEQ ID NO 113

&lt;211&gt; LENGTH: 119

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 113

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

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Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Thr His Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Ile Tyr Thr Gly Arg Trp Val Pro Phe Glu Tyr Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 114  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 114

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Thr Asp Ala Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 115  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 115

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Lys Tyr  
20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly  
100 105 110

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Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 116  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 116

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Leu Lys Tyr  
20 25 30  
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 117  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 117

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Lys Tyr  
20 25 30  
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Ser Gln Ile Ala Asp Thr Gly Asp Arg Arg Tyr Tyr Asp Asp Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 118  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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&lt;400&gt; SEQUENCE: 118

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asp Thr Ala Asp Arg Arg Tyr Tyr Asp Asp Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

&lt;210&gt; SEQ ID NO 119

&lt;211&gt; LENGTH: 119

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 119

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asp Thr Gly Asp Arg Arg Tyr Tyr Asp His Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

&lt;210&gt; SEQ ID NO 120

&lt;211&gt; LENGTH: 119

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 120

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

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Ser Gln Ile Ser Asp Thr Gly Asp Arg Arg Tyr Tyr Asp Asp Ala Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 121  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 121

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Lys Tyr  
 20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gln Ile Ala Asp Thr Ala Asp Arg Arg Tyr Tyr Asp Asp Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 122  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 122

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Lys Tyr  
 20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gln Ile Ala Asp Thr Gly Asp Arg Arg Tyr Tyr Asp His Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly

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100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 123  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 123

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Lys Tyr  
20 25 30  
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Ser Gln Ile Ala Asp Thr Gly Asp Arg Arg Tyr Tyr Asp Asp Ala Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly  
100 105 110  
Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 124  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 124

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15  
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
20 25 30  
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45  
Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val  
50 55 60  
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80  
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95  
Ala Ile Tyr Thr Gly Arg Trp Gly Pro Phe Val Tyr Trp Gly Gln Gly  
100 105 110  
Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 125  
<211> LENGTH: 119  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:

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<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 125

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Ile Tyr Thr Gly Arg Trp Val Pro Phe Ala Tyr Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 126

<211> LENGTH: 119

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 126

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
35 40 45

Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val  
50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
85 90 95

Ala Ile Tyr Thr Gly Arg Trp Gly Pro Phe Gln Tyr Trp Gly Gln Gly  
100 105 110

Thr Leu Val Thr Val Ser Ser  
115

<210> SEQ ID NO 127

<211> LENGTH: 119

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 127

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val

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      35          40          45
Ser  Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val
   50          55          60
Lys  Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
   65          70          75          80
Leu  Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
           85          90          95
Ala  Ile Tyr Thr Gly Arg Trp Glu Pro Phe Gln Tyr Trp Gly Gln Gly
           100          105          110
Thr  Leu Val Thr Val Ser Ser
           115

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<210> SEQ ID NO 128
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 128

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
  1          5          10          15
Ser  Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr
           20          25          30
Ser  Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
           35          40          45
Ser  Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val
           50          55          60
Lys  Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
           65          70          75          80
Leu  Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
           85          90          95
Ala  Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly
           100          105          110
Thr  Leu Val Thr Val Ser Ser
           115

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<210> SEQ ID NO 129
<211> LENGTH: 119
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 129

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
  1          5          10          15
Ser  Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr
           20          25          30
Ser  Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
           35          40          45
Ser  Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val
           50          55          60
Lys  Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
           65          70          75          80
Leu  Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
           85          90          95

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Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Gln Tyr Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 130  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 130

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Ile Tyr Thr Gly Arg Trp Val Pro Phe Gln Tyr Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 131  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 131

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gln Ile Ser Asp Thr Gly Asp Arg Arg Tyr Tyr Asp His Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 132  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence

-continued

<220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 132

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Leu Lys Tyr
 20           25           30
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35           40           45
Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val
 50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65           70           75           80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85           90           95
Ala Ile Tyr Thr Gly Arg Trp Val Pro Phe Glu Tyr Trp Gly Gln Gly
 100          105          110
Thr Leu Val Thr Val Ser Ser
 115
  
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<210> SEQ ID NO 133  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 133

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Lys Tyr
 20           25           30
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35           40           45
Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val
 50           55           60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65           70           75           80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85           90           95
Ala Ile Tyr Thr Gly Arg Trp Val Pro Phe Glu Tyr Trp Gly Gln Gly
 100          105          110
Thr Leu Val Thr Val Ser Ser
 115
  
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<210> SEQ ID NO 134  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 134

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Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1           5           10           15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Leu Lys Tyr
 20           25           30
  
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Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 137  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 137

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Leu Lys Tyr  
 20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Asp His Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Ile Tyr Thr Gly Arg Trp Glu Pro Phe Val Tyr Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 138  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 138

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Leu Lys Tyr  
 20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Ser His Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Ile Tyr Thr Gly Arg Trp Val Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 139  
 <211> LENGTH: 119  
 <212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 139

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Ser His Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Val Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 140  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 140

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Thr His Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Val Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 141  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 141

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Leu Lys Tyr  
 20 25 30

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Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Thr His Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Ile Tyr Thr Gly Arg Trp Val Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 142  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 142

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Lys Tyr  
 20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110

Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 143  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 143

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Leu Lys Tyr  
 20 25 30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val  
 50 55 60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys

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85	90	95
Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly		
100	105	110
Thr Leu Val Thr Val Ser Ser		
115		

<210> SEQ ID NO 144  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 144

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly		
1	5	10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Leu Lys Tyr		
20	25	30
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val		
35	40	45
Ser Gln Ile Ser Asp Thr Gly Asp Arg Arg Tyr Tyr Asp His Ser Val		
50	55	60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr		
65	70	75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys		
85	90	95
Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly		
100	105	110
Thr Leu Val Thr Val Ser Ser		
115		

<210> SEQ ID NO 145  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 145

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly		
1	5	10 15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr		
20	25	30
Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val		
35	40	45
Ser Gln Ile Ala Asp Thr Ala Asp Arg Thr Tyr Tyr Ala His Ser Val		
50	55	60
Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr		
65	70	75 80
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys		
85	90	95
Ala Ile Tyr Thr Gly Arg Trp Val Pro Phe Glu Tyr Trp Gly Gln Gly		
100	105	110
Thr Leu Val Thr Val Ser Ser		
115		

<210> SEQ ID NO 146  
 <211> LENGTH: 119

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<212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 146

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ser Asp Thr Ala Asp Arg Thr Tyr Tyr Ala His Ala Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Val Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 147  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 147

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ala Asp Thr Ala Asp Arg Thr Tyr Tyr Asp His Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Val Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 148  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 148

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr





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<211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 153

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ala Asp Thr Ala Asp Arg Arg Tyr Tyr Asp His Ala Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 154  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 154

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15  
 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Val Lys Tyr  
 20 25 30  
 Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45  
 Ser Gln Ile Ala Asp Thr Ala Asp Arg Arg Tyr Tyr Asp His Ser Val  
 50 55 60  
 Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80  
 Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95  
 Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly  
 100 105 110  
 Thr Leu Val Thr Val Ser Ser  
 115

<210> SEQ ID NO 155  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 155

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15



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Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                   85                                  90                                  95

Ala Lys Tyr Thr Gly Arg Trp Glu Pro Phe Glu Tyr Trp Gly Gln Gly  
                   100                                  105                                  110

Thr Leu Val Thr Val Ser Ser  
                   115

<210> SEQ ID NO 158  
 <211> LENGTH: 119  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 158

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1                  5                                  10                                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Phe Lys Tyr  
                   20                                  25                                  30

Ser Met Gly Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
                   35                                  40                                  45

Ser Gln Ile Ser Asp Thr Gly Asp Arg Arg Tyr Tyr Asp His Ser Val  
                   50                                  55                                  60

Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
                   65                                  70                                  75                                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
                   85                                  90                                  95

Ala Ile Tyr Thr Gly Arg Trp Ala Pro Phe Glu Tyr Trp Gly Gln Gly  
                   100                                  105                                  110

Thr Leu Val Thr Val Ser Ser  
                   115

<210> SEQ ID NO 159  
 <211> LENGTH: 360  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 159

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60  
 tcctgtgcag cctccggatt cacctttatg aggtatagga tgcattgggt ccgccaggct 120  
 ccaggggaagg gtctagagtg ggtctcatcg attgattcta atggttctag tacatactac 180  
 gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240  
 ctgcaaatga acagcctgcg tgccgaggac acccggtat attactgtgc gaaagatcgt 300  
 accgagcgtt cgccggtttt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

<210> SEQ ID NO 160  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 160

gaggtgcagc tgttggagtc tgggggaggc ttggtgcagc ctggggggtc cctgcgtctc 60  
 tcctgtgcag cctccggatt cacctttggt gattatgaga tgcattgggt ccgccaggct 120

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ccaggggaagg gtctagagtg ggtctcatct attagtgaga gtggtacgac gacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaacgctcg 300
ttttctgctt ctacgtttga ctactggggt cagggaaacc tggtcaccgt ctcgagc 357

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<210> SEQ ID NO 161
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 161

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct 120
ccaggggaagg gtctagagtg ggtctcacag atttcgaata cgggtgggtca tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatacg 300
ggtcattggg agccttttga ctactggggt cagggaaacc tggtcaccgt ctcgagc 357

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<210> SEQ ID NO 162
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 162

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct 120
ccaggggaagg gtctagagtg ggtctcacag atttcgaata cgggtgggtca tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatacg 300
ggtcgttggg agccttatga ctactggggt cagggaaacc tggtcaccgt ctcgagc 357

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<210> SEQ ID NO 163
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 163

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct 120
ccaggggaagg gtctagagtg ggtctcacag atttcgaata cgggtgggtca tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatacg 300
ggtcgttggg agccttttga ctactggggt cagggaaacc tggtcaccgt ctcgagc 357

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<210> SEQ ID NO 164
<211> LENGTH: 357
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 164

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tctctgtcag cctccggatt cacctttggt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgggtca tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatacg	300
ggtcgttggg agccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 165  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 165

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tctctgtcag cctccggatt cacctttggt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac	180
gcacacgcgg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gatatact	300
gggcgttggg tgccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 166  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 166

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tctctgtcag cctccggatt cacctttggt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgggtca tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatatact	300
ggtcgttggg agccttttga ctactggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 167  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 167

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tctctgtcag cctccggatt cacctttggt aagtattcga tgggatgggt ccgccaggct	120
ccagggaaag gtccagagtg ggtctcacag atttcgaata cgggtgggtca tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240

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ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcgttggg agccttttga ctactggggt cagggaaacc tggtcacagt ctcgagc 357

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<210> SEQ ID NO 168
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 168
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtggg cccagcaggct 120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgggtca tacatactac 180
gcagactcog tgaagggccg gttcaccata tcccgcgaca attccaagaa cacgctgtat 240
atgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcgttggg agccttttga ctactggggt cagggaaacc tggtcacagt ctcgagc 357

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<210> SEQ ID NO 169
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 169
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtggg cccagcaggct 120
ccagggaaagg atctagagtg ggtctcacag atttcgaata cgggtgggtca tacatactac 180
gcagactcog tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcgttggg agccttttga ctactggggt cagggaaacc tggtcacagt ctcgagc 357

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<210> SEQ ID NO 170
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 170
gaggtgcagc tgttggagtc agggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtggg cccagcaggct 120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgggtca tacatactac 180
gcagactcog tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatataatcg 300
ggtcgttggg agccttttga ccaactggggt caggggaaacc tggtcacagt ctcgagc 357

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<210> SEQ ID NO 171
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 171

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatca tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatacg	300
ggtcgttggg agccttttga ctactgggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 172

<211> LENGTH: 357

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 172

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatatacg	300
ggtcgttggg agccttttga ctactgggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 173

<211> LENGTH: 357

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 173

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg	300
ggtcgttggg agccttttga ctactgggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 174

<211> LENGTH: 357

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 174

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatca tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg	300
ggtcgttggg agccttttga ctactgggggt cagggaaacc tggtcaccgt ctcgagc	357

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<210> SEQ ID NO 175  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 175

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tctctgtcag cctccggatt cacctttgtt aagtattcga tgggatgggt ccgccaggct	120
ccagggaaag gtccagagtg ggtctcacag atttcgaata cgggtgatcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggat attactgtgc gatataatcg	300
ggtcgttggg agccttttga ctactggggg cagggaaacc tggtcacagt ctcgagc	357

<210> SEQ ID NO 176  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 176

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tctctgtcag cctccggatt cacctttgtt aagtattcga tgggatgggt ccgccaggct	120
ccagggaaag gtccagagtg ggtctcacag atttcgaata cgggtgatca tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggat attactgtgc gatataatcg	300
ggtcgttggg agccttttga ctactggggg cagggaaacc tggtcacagt ctcgagc	357

<210> SEQ ID NO 177  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 177

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tctctgtcag cctccggatt cacctttgtt aagtattcga tgggggggggt ccgccaggct	120
ccagggaagg atctagagtg ggtctcacag atttcgaata cgggtgatcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggat attactgtgc gatataatcg	300
ggtcgttggg agccttttga ctactggggg cagggaaacc tggtcacagt ctcgagc	357

<210> SEQ ID NO 178  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 178

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
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tccctgtgcag cctccggatt cacctttggt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatca tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg	300
ggtcgttggg agccttttga ctactggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 179  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 179

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tccctgtgcag cctccggatt cacctttggt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg	300
ggtcgttggg agccttttgt ctactggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 180  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 180

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tccctgtgcag cctccggatt cacctttggt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gatataatcg	300
ggtcgttggg agccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 181  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 181

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tccctgtgcag cctccggatt cacctttggt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatcg tacatactac	180
gcggactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gatataatcg	300
ggtcgttgga agccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 182  
 <211> LENGTH: 357

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<212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 182

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gatatact	300
gggcgttggg tgccttttga gtactgggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 183  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 183

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatcg tacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatatact	300
ggtcgttggg ggccttttga gtactgggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 184  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 184

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatcg tagatactac	180
gcagactctg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggcat attactgtgc gatatact	300
ggtcgttggg agccttttga ctactgggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 185  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 185

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata ctgctgatcg tacatactac	180

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```
gcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcggttggg agccttttaa ctactggggt cagggaaacc tggtcaccgt ctcgagc 357
```

```
<210> SEQ ID NO 186
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.
```

```
<400> SEQUENCE: 186
```

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgctctc 60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct 120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatcg tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcggttggg cgccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc 357
```

```
<210> SEQ ID NO 187
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.
```

```
<400> SEQUENCE: 187
```

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgctctc 60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct 120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatcg tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa ctgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcggttggg tgccttttga caactggggt cagggaaacc tggtcaccgt ctcgagc 357
```

```
<210> SEQ ID NO 188
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.
```

```
<400> SEQUENCE: 188
```

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgctctc 60
tcctgtgcag cctccggatt cacctttatt acgtattcga tgggggtgggt ccgccaggct 120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatcg tacatactac 180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcggttggg agccttttca gtactggggt cagggaaacc tggtcaccgt ctcgagc 357
```

```
<210> SEQ ID NO 189
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.
```

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&lt;400&gt; SEQUENCE: 189

```

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt cacctttggt aagtattcga tgggggtgggt ccgccaggct   120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatcg tacatactac   180
gcggactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg   300
ggtcgttggg agccttttga ctactggggt cagggaaacc tggtcaccgt ctcgagc     357

```

&lt;210&gt; SEQ ID NO 190

&lt;211&gt; LENGTH: 357

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 190

```

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt cacctttttt aagtattcga tgggggtgggt ccgccaggct   120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatcg tacatactac   180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaagac accgcggtat attactgtgc gatataatcg   300
ggtcgttggg agccttttga ctactggggt cagggaaacc tggtcaccgt ctcgagc     357

```

&lt;210&gt; SEQ ID NO 191

&lt;211&gt; LENGTH: 357

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 191

```

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt cacctttggt aagtattcga tgggggtgggt ccgccagggt   120
ccagggaaagg gtctagagtg ggtctcacag atttcggata cgggtgatcg tagatactac   180
gatgactctg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg   300
ggtcgttggg agccttttga ctactggggt cagggaaacc tggtcaccgt ctcgagc     357

```

&lt;210&gt; SEQ ID NO 192

&lt;211&gt; LENGTH: 357

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 192

```

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt cacctttggt aagtattcga tgggggtgggt ccgccagggt   120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatcg tagatactac   180
gcagacgcgg tgaaggggcg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg   300

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 ggtcgttggg agccttttga ctactggggg cagggaaacc tggtcaccgt ctcgagc 357

<210> SEQ ID NO 193  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 193

gaggtgcagc tgttgagtc tgggggagc ttggtacagc ctggggggtc cctgcgtctc 60  
 tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtggg cgcaggct 120  
 ccaggaagg gtctagagtg ggtctcacag atttcaata cgggtgatcg tacatactac 180  
 gcagactcgc tgaagggcgc gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240  
 ctgcaaatga acagcctgcg tgctgaggac accgcggat attactgtgc gatatactac 300  
 ggtcgttggg agccttttaa gtactggggg cagggaaacc tggtcaccgt ctcgagc 357

<210> SEQ ID NO 194  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 194

gaggtgcagc tgttgagtc tgggggagc ttggtacagc ctggggggtc cctgcgtctc 60  
 tcctgtgcag cctccggatt cacctttagt aagtattcga tgggggtggg cgcaggct 120  
 ccaggaagg gtctagagtg ggtctcacag atttcaata cgggtgagcg tagatactac 180  
 gcagactcag tgaagggcgc gttcaccatc tcccgcgaca atccaagaa cacgctgtat 240  
 ctgcaaatga acagcctgcg tgccgaggac accgcggat attactgtgc gatatactac 300  
 ggtcggtggg agccttttga atactggggg cagggaaacc tggtcaccgt ctcgagc 357

<210> SEQ ID NO 195  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 195

gaggtgcagc tgttgagtc tgggggagc ttggtacagc ctggggggtc cctgcgtctc 60  
 tcctgtgcag cctccggatt cacctttgtt aactattcga tgggggtggg cgcaggct 120  
 ccaggaagg gtctagagtg ggtctcacag atttcaata cgggtgatcg tacatactac 180  
 gcgactcgc tgaagggcgc gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240  
 ctgcaaatga acagcctgcg tgccgaggac accgcggat attactgtgc gatatactac 300  
 ggtcgttggg agccttatga gtactggggg cagggaaacc tggtcaccgt cagagc 357

<210> SEQ ID NO 196  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 196

gaggtgcagc tgttgagtc tgggggagc ttggtacagc ctggggggtc cctgcgtctc 60

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tctctgtgcag cctccggatt cacctttggt aagtattcga tgggggtgggt cgcagcagct 120
ccaggggaagg gtctagagtg ggtctcacag attgcgaata cgggtgatcg tagatactac 180
gcagactctg tgaagggccg gttcaccatc tcccgcgata attccaagaa cacactgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataacg 300
ggtcgttggg agccttttgt ctactggggt cagggaaacc tggtcaccgt ctcgagc 357

```

```

<210> SEQ ID NO 197
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 197

```

```

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgctctc 60
tctctgtgcag cctccggatt cacctttggt aagtattcga tgggggtgggt cgcagcagct 120
ccaggggaagg gtctagagtg ggtctcacag attgcgaata cgggtgatcg tagatactac 180
gcagactctg tgaagggccg gttcaccatc tcccgcgata attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataacg 300
ggtcgttgga agccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc 357

```

```

<210> SEQ ID NO 198
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 198

```

```

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgctctc 60
tctctgtgcag cctccggatt cacctttggt aagtattcga tgggggtgggt cgcagcagct 120
ccaggggaagg gtctagagtg ggtctcacag attgcgaata cgggtgatcg tagatactac 180
gcagactctg tgaagggccg gttcaccatc tcccgcgata attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gatataact 300
gggcgttggg tgccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc 357

```

```

<210> SEQ ID NO 199
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 199

```

```

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgctctc 60
tctctgtgcag cctccggatt cacctttggt aagtattcga tgggggtgggt cgcagcagct 120
ccaggggaagg gtctagagtg ggtctcacag attgcgaata cgggtgatcg tagatactac 180
gcagactctg tgaagggccg gttcaccatc tcccgcgata attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataacg 300
ggtcgttgga ggccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc 357

```

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<210> SEQ ID NO 200

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<211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 200

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tctctgtcag cctccgatt cacctttgt aagtattcga tgggggtgggt ccgccaggct	120
ccaggggaagg gtctagagtg ggtctcacag attgcgaata cgggtgatcg tagatactac	180
gcagactctg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac acccggtat attactgtgc gatataatcg	300
ggtcggtggg gccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 201  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 201

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tctctgtcag cctccgatt cacctttgt aagtattcga tgggggtgggt ccgccaggct	120
ccaggggaagg gtctagagtg ggtctcacag atttcaata ctgctgatcg tacatactac	180
gcacactcag tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac acccggtat attactgtgc ggtataatcg	300
ggtcggtggg agccttttga ctactggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 202  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 202

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tctctgtcag cctccgatt cacctttgt aagtattcga tgggggtgggt ccgccaggct	120
ccaggggaagg gtctagagtg ggtctcacag atttcaata ctgctgatcg tacatactac	180
gcacactcag tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgctgaggac acccggtat attactgtgc gatataatcg	300
ggtcggttga agccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 203  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 203

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tctctgtcag cctccgatt cacctttgt aagtattcga tgggggtgggt ccgccaggct	120
ccaggggaagg gtctagagtg ggtctcacag atttcaata ctgctgatcg tacatactac	180

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gcacactcgc tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gatataact 300
ggcgcttggg tgccttttga gtactggggc cagggaaacc tggtcaccgt ctcgagc 357

```

```

<210> SEQ ID NO 204
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 204

```

```

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggggtggg cccagcagct 120
ccaggaagg gtctagagtg ggtctcacag atttcgaata ctgctgatcg tacatactac 180
gcacactcgc tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataact 300
ggcgcttggg tgccttttga gtactggggc cagggaaacc tggtcaccgt ctcgagc 357

```

```

<210> SEQ ID NO 205
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 205

```

```

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggggtggg cccagcagct 120
ccaggaagg gtctagagtg ggtctcacag atttcgaata ctgctgatcg tacatactac 180
gcacactcgc tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataact 300
ggcgcttggg tgccttttga gtactggggc cagggaaacc tggtcaccgt ctcgagc 357

```

```

<210> SEQ ID NO 206
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 206

```

```

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggggtggg cccagcagct 120
ccaggaagg gtctagagtg ggtctcacag atttcggata cgggtgatcg tagatactac 180
gatgactctg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataact 300
ggcgcttggg agccttttgt ctactggggc cagggaaacc tggtcaccgt ctcgagc 357

```

```

<210> SEQ ID NO 207
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 207

```

gaggtgcagc tgttgagtc tgggggagc ttggtacagc ctggggggtc cctgcgtctc    60
tcctgtgcag cctccgatt caccttgtt aagtattcga tgggggtggg cccagggcc    120
ccaggaagg gtctagagtg ggtctcacag atttcggata cgggtgatcg tagatactac    180
gatgactctg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat    240
ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gatataatcg    300
ggtcgttggg agccttttga gtactggggg caggaaccct tggtcaccgt ctcgagc    357

```

&lt;210&gt; SEQ ID NO 208

&lt;211&gt; LENGTH: 357

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 208

```

gaggtgcagc tgttgagtc tgggggagc ttggtacagc ctggggggtc cctgcgtctc    60
tcctgtgcag cctccgatt caccttgtt aagtattcga tgggggtggg cccagggct    120
ccaggaagg gtctagagtg ggtctcacag atttcggata cgggtgatcg tagatactac    180
gatgactctg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat    240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg    300
gggcgttggg tgccttttga gtactggggg caggaaccct tggtcaccgt ctcgagc    357

```

&lt;210&gt; SEQ ID NO 209

&lt;211&gt; LENGTH: 357

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 209

```

gaggtgcagc tgttgagtc tgggggagc ttggtacagc ctggggggtc cctgcgtctc    60
tcctgtgcag cctccgatt caccttgtt aagtattcga tgggggtggg cccagggct    120
ccaggaagg gtctagagtg ggtctcacag atttcggata cgggtgatcg tagatactac    180
gatgactctg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat    240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg    300
ggtcgttggg ggccttttga gtactggggg caggaaccct tggtcaccgt ctcgagc    357

```

&lt;210&gt; SEQ ID NO 210

&lt;211&gt; LENGTH: 357

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 210

```

gaggtgcagc tgttgagtc tgggggagc ttggtacagc ctggggggtc cctgcgtctc    60
tcctgtgcag cctccgatt caccttgtt aagtattcga tgggggtggg cccagggct    120
ccaggaagg gtctagagtg ggtctcacag atttcggata cgggtgatcg tagatactac    180
gatgactctg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat    240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg    300

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ggtcggtggg gccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc 357

<210> SEQ ID NO 211  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 211

gaggtgcagc tgttgagtc tgggggagc ttggtacagc ctggggggtc cctgcgtctc 60  
 tcctgtgcag cctccgatt caccttgggt aagattcga tgggggtgggt ccgccaggct 120  
 ccaggaagg gtctagagt ggtctcacag atttcgaata cgggtgatcg tagatactac 180  
 gcagacgcgg tgaagggcg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240  
 ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatatactac 300  
 ggtcgttggg agccttttgt ctactggggt cagggaaacc tggtcaccgt ctcgagc 357

<210> SEQ ID NO 212  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 212

gaggtgcagc tgttgagtc tgggggagc ttggtacagc ctggggggtc cctgcgtctc 60  
 tcctgtgcag cctccgatt caccttgggt aagattcga tgggggtgggt ccgccaggct 120  
 ccaggaagg gtctagagt ggtctcacag atttcgaata cgggtgatcg tagatactac 180  
 gcagacgcgg tgaagggcg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240  
 ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gatatactac 300  
 ggtcgttggg agccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc 357

<210> SEQ ID NO 213  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 213

gaggtgcagc tgttgagtc tgggggagc ttggtacagc ctggggggtc cctgcgtctc 60  
 tcctgtgcag cctccgatt caccttgggt aagattcga tgggggtgggt ccgccaggcc 120  
 ccaggaagg gtctagagt ggtctcacag atttcgaata cgggtgatcg tagatactac 180  
 gcagacgcgg tgaagggcg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240  
 ctgcaaatga acagcctgcg tgccgaagac accgcggtat attactgtgc gatatactac 300  
 gggcggttggg gccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc 357

<210> SEQ ID NO 214  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 214

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gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct   120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatcg tagatactac   180
gcagacgcgg tgaagggcg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg   300
ggtcgttggg ggccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc   357

```

```

<210> SEQ ID NO 215
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 215

```

```

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct   120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatcg tagatactac   180
gcagacgcgg tgaagggcg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg   300
ggtcgttggg ggccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc   357

```

```

<210> SEQ ID NO 216
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 216

```

```

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt caccttttgg aagtattcga tgggggtgggt ccgccaggct   120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatcg tagatactac   180
gcagactctg tgaagggcgg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg   300
ggtcgttggg ggccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc   357

```

```

<210> SEQ ID NO 217
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 217

```

```

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt caccttttgg aagtattcga tgggggtgggt ccgccaggct   120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata ctgctgatcg tacatactac   180
gcacactcgg tgaagggcgg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg   300
ggtcgttggg ggccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc   357

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<210> SEQ ID NO 218  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 218

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccgatt caccttttc aagtattcga tggggtggt cgcagcaggct	120
ccaggaagg gtctagagt ggtctcacag atttcggata cgggtgatcg tagatactac	180
gatgactctg tgaagggcgc gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggat attactgtgc gatatactacg	300
ggtcgttggg agccttttgt ctactggggt caggaaccc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 219  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 219

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccgatt caccttttg aagtattcga tggggtggt cgcagcaggct	120
ccaggaagg gtctagagt ggtctcacag atttcggata cgggtgatcg tagatactac	180
gatgactctg tgaagggcgc gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggat attactgtgc gatatactacg	300
ggtcgttggg agccttttgt ctactggggt caggaaccc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 220  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 220

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttgt aagtattcga tggggtggt cgcagcaggct	120
ccaggaagg gtctagagt ggtctcacag attgcgaata cgggtgatcg tagatactac	180
gcagactctg tgaagggcgc gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggcat attactgtgc gatatactacg	300
ggtcgttggc cgcacttga ctactggggt caggaaccc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 221  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 221

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttgt aagtattcga tggggtggt cgcagcaggct	120

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```

ccaggggaagg gtctagagtg ggtctcacag attgcgaata cgggtgatcg tagatactac 180
gcagactctg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggcat attactgtgc gatataatcg 300
ggtcggtggc cgcacttga gtactggggt cagggaaacc tggtcaccgt ctcgagc 357

```

```

<210> SEQ ID NO 222
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 222

```

```

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggggtggg cgcaccaggct 120
ccaggggaagg gtctagagtg ggtctcacag atttcgaata ctgctgatcg tacatactac 180
gcacactcgc tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcgggat attactgtgc gatataatcg 300
ggtcggtggc cgcacttga ctactggggt cagggaaacc tggtcaccgt ctcgagc 357

```

```

<210> SEQ ID NO 223
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 223

```

```

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggggtggg cgcaccaggct 120
ccaggggaagg gtctagagtg ggtctcacag atttcgaata ctgctgatcg tacatactac 180
gcacactcgc tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcgggat attactgtgc gatataatcg 300
ggtcggtggc cgcacttga gtactggggt cagggaaacc tggtcaccgt ctcgagc 357

```

```

<210> SEQ ID NO 224
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 224

```

```

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggggtggg cgcaccaggct 120
ccaggggaagg gtctagagtg ggtctcacag atttcggata cgggtgatcg tagatactac 180
gatgactctg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcgggat attactgtgc gatataatcg 300
ggtcggtggc cgcacttga ctactggggt cagggaaacc tggtcaccgt ctcgagc 357

```

```

<210> SEQ ID NO 225
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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<220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 225

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgctctc	60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggggggtt ccgccaggct	120
ccagggaaag gtctagagtg ggtctcacag atttcggata cgggtgatcg tagatactac	180
gatgactctg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcgggat attactgtgc gatataatcg	300
ggtcggtggc ccgactttga gtactggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 226  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 226

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgctctc	60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggatgggt ccgccaggct	120
ccagggaaag gtccagagtg ggtctcacag atttcggcct ggggtgacag gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcgggat attactgtgc gatataatcg	300
ggtcggtggg agccttttga ctactggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 227  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 227

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgctctc	60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggggggtt ccgccaggct	120
ccagggaaag gtccagagtg ggtctcacag atttcggacg gcggtcagag gacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcgggat attactgtgc gatataatcg	300
ggtcggtggg agccttttga ctactggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 228  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 228

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgctctc	60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggatgggt ccgccaggct	120
ccagggaaag gtccagagtg ggtctcacag atttcggact ccggttaccg cacatactac	180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240

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```
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcgttggg agccttttga ctactggggt cagggaaacc tggtcaccgt ctcgagc 357
```

```
<210> SEQ ID NO 229
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.
```

```
<400> SEQUENCE: 229
```

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tggggtgggt ccgccaggct 120
ccagggaaag gtccagagtg ggtctcacag atttcggacg ggggtacgcg gacatactac 180
gcagactcgg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcgttggg agccttttga ctactggggt cagggaaacc tggtcaccgt ctcgagc 357
```

```
<210> SEQ ID NO 230
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.
```

```
<400> SEQUENCE: 230
```

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggatgggt ccgccaggct 120
ccagggaaaag gtccagagtg ggtctcacag atttcggaca agggtacgcg cacatactac 180
gcagactcgg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcgttggg agccttttga ctactggggt cagggaaacc tggtcaccgt ctcgagc 357
```

```
<210> SEQ ID NO 231
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.
```

```
<400> SEQUENCE: 231
```

```
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggatgggt ccgccaggct 120
ccagggaaaag gtccagagtg ggtctcacag atttcggaga ccggtcgcag gacatactac 180
gcagactcgg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcgttggg agccttttga ctactggggt cagggaaacc tggtcaccgt ctcgagc 357
```

```
<210> SEQ ID NO 232
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.
```

```
<400> SEQUENCE: 232
```

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```

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct   120
ccagggaaagg gtctagagtg ggtctcacag attaacaata cgggttcgac cacatactac   180
gcagactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg   300
ggtcgttggg agccttttga ctactggggg cagggaaacc tggtcaccgt ctcgagc   357

```

```

<210> SEQ ID NO 233
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 233

```

```

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct   120
ccagggaaagg gtccagagtg ggtctcacag atttcgaata ctgctgatcg tacatactac   180
gcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gatataatcg   300
gggcgttggg tgccttttga gtactggggg cagggaaacc tggtcaccgt ctcgagc   357

```

```

<210> SEQ ID NO 234
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 234

```

```

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct   120
ccagggaaagg gtccagagtg ggtctcacag atttcgaata ctgctgatcg tacatactac   180
gcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg   300
ggtcgttggg cgccttttga gtactggggg cagggaaacc tggtcaccgt ctcgagc   357

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<210> SEQ ID NO 235
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 235

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct   120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac   180
gcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gatataatcg   300
gggcgttggg tgccttttga gtactggggg cagggaaacc tggtcaccgt ctcgagc   357

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<210> SEQ ID NO 236  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 236

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac	180
gcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg	300
ggtcgggtggg cgccttttga gtactgggggt cagggaaacc ttggtcaccgt ctcgagc	357

<210> SEQ ID NO 237  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 237

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac	180
gatgactctg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg	300
ggtcgttggg ggccttttga gtactgggggt cagggaaacc ttggtcaccgt ctcgagc	357

<210> SEQ ID NO 238  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 238

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac	180
acacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg	300
ggtcgggtggg cgccttttga gtactgggggt cagggaaacc ttggtcaccgt ctcgagc	357

<210> SEQ ID NO 239  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 239

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120

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ccaggggaagg gtctagagtg ggtctcacag atttccaata ctgctgatcg cagatactac 180
gcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcgggtggg cgccttttga gtactggggg caggggaacc tggtcaccgt ctcgagc 357

```

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<210> SEQ ID NO 240
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 240

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct 120
ccaggggaagg gtctagagtg ggtctcacag attttgaata ctgctgatcg tacatactac 180
gatcactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcgggtggg cgccttttga gtactggggg caggggaacc tggtcaccgt ctcgagc 357

```

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<210> SEQ ID NO 241
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 241

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct 120
ccaggggaagg gtctagagtg ggtctcacag atttccaata ctgctgatcg tacatactac 180
gatcactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcgggtggg cgccttttga gtactggggg caggggaacc tggtcaccgt ctcgagc 357

```

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<210> SEQ ID NO 242
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 242

```

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct 120
ccaggggaagg gtctagagtg ggtctcacag atttccgata ctgctgatcg tagatactac 180
gcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcgggtggg cgccttttga gtactggggg caggggaacc tggtcaccgt ctcgagc 357

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<210> SEQ ID NO 243
<211> LENGTH: 357
<212> TYPE: DNA

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<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 243
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt cacctttggt aagtattcga tgggggtgggt ccgccaggct   120
ccagggaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tagatactac   180
gatcactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg   300
ggtcggtggg cgccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc     357

```

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<210> SEQ ID NO 244
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 244
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt cacctttggt aagtattcga tgggggtgggt ccgccaggct   120
ccagggaagg gtctagagtg ggtctcacag atttcgaata ctgctgatcg tacatactac   180
gcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggtatatact   300
gggcggttggg tgtcttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc     357

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<210> SEQ ID NO 245
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 245
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt cacctttggt aagtattcga tgggggtgggt ccgccaggct   120
ccagggaagg gtctagagtg ggtctcacag atttcgaata ctgctgatcg tacatactac   180
gcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gctatatact   300
gggcggttggg tgtcttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc     357

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<210> SEQ ID NO 246
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 246
gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt cacctttggt aagtattcga tgggggtgggt ccgccaggct   120
ccagggaagg gtctagagtg ggtctcacag atttcgaata ctgctgatcg tacatactac   180
gcacactccg tgaagggccg gtttaccatc tcccgcgaca attccaagaa cacgctgtat   240

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ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc ggtatatact 300
gggcgttggg tgccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc 357

```

```

<210> SEQ ID NO 247
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 247

```

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtggg cgcaccaggct 120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata ctgctgatcg tacatactac 180
gcacactcog tgaagggcog gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gctatatact 300
gggcgttggg tgccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc 357

```

```

<210> SEQ ID NO 248
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 248

```

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtggg cgcaccaggct 120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata ctgctgatcg tagatactac 180
gcacactcog tgaagggcog gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatatactac 300
ggtcggttggg cgccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc 357

```

```

<210> SEQ ID NO 249
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 249

```

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gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtggg cgcaccaggct 120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata ctgctgatcg tagatactac 180
gcagacgcgg tgaagggcog gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatatactac 300
ggtcggttggg agccttttgt ctactggggt cagggaaacc tggtcaccgt ctcgagc 357

```

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<210> SEQ ID NO 250
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 250

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcgg cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggcatcg tagatactac	180
gcacacgcgg tgaaggggcg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg	300
ggtcgttggg agccttttgt ctactgggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 251

<211> LENGTH: 357

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 251

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata ctgctgatcg tagatactac	180
gcagacgcgg tgaaggggcg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg	300
ggtcgttggg agccttttgt ctactgggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 252

<211> LENGTH: 357

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 252

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata cgggtgatcg tagatactac	180
gcacacgcgg tgaaggggcg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg	300
ggtcgttggg agccttttgt ctactgggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 253

<211> LENGTH: 357

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 253

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcgaata ctgctgatcg tagatactac	180
gcacacgcgg tgaaggggcg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg	300
ggtcgttggg agccttttgt ctactgggggt cagggaaacc tggtcaccgt ctcgagc	357

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<210> SEQ ID NO 254  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 254

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tctctgtcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag attgcgaata cggctgatcg tagatactac	180
gcacacgcgg tgaaggggcg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggat attactgtgc gatataacg	300
ggtcgttggg agccttttgt ctactgggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 255  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 255

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tctctgtcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag attgtgaata cgggtgatcg tagatactac	180
gcagacgcgg tgaaggggcg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggat attactgtgc gatataacg	300
ggtcgttggg agccttttgt ctactgggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 256  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 256

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tctctgtcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag attgcgaata cgggtgatcg tagatactac	180
gcagacgcgg tgaaggggcg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggat attactgtgc gatataacg	300
ggtcgttggg agccttttgt ctactgggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 257  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 257

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
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tccctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac	180
gatcactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg	300
ggtcggtggg cgccttttga gtactggggg cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 258  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 258

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tccctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac	180
gatcactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg	300
ggtcggttggg ggccttttga gtactggggg cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 259  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 259

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tccctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac	180
gatcactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg	300
ggtcggttggg agccttttgt ctactggggg cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 260  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 260

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tccctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac	180
tcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gatataatcg	300
gggcggttggg tgccttttga gtactggggg cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 261  
 <211> LENGTH: 357

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<212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 261

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac	180
acacactccg tgaagggcgc gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgctgaggac accgcggat attactgtgc gatatact	300
gggcgttggg tgccttttga gtactggggc cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 262  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 262

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac	180
acagacgcgg tgaagggcgc gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggat attactgtgc gatatact	300
ggtcgttggg agccttttgt ctactggggc cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 263  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 263

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttttc aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac	180
gcacactccg tgaagggcgc gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggat attactgtgc gatatact	300
ggtcggttggg cgccttttga gtactggggc cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 264  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 264

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt cacctttttg aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac	180

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```
gcacactcgc tgaagggcgc gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcggtggg gccttttga gtactggggt caggaaccc tggtcaccgt ctcgagc 357
```

```
<210> SEQ ID NO 265
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.
```

```
<400> SEQUENCE: 265
gaggtgcagc tgttgagtc tggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccgatt caccttttc aagtattcga tggggtgggt ccgccaggct 120
ccaggaagg gtctagagt ggtctcacag attcggata cgggtgatcg tagatactac 180
gatgactctg tgaagggcgc gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcggtggg gccttttgt ctactggggt caggaaccc tggtcaccgt ctcgagc 357
```

```
<210> SEQ ID NO 266
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.
```

```
<400> SEQUENCE: 266
gaggtgcagc tgttgagtc tggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccgatt caccttttc aagtattcga tggggtgggt ccgccaggct 120
ccaggaagg gtctagagt ggtctcacag attcggata ctgctgatcg tagatactac 180
gatgactctg tgaagggcgc gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcggtggg gccttttgt ctactggggt caggaaccc tggtcaccgt ctcgagc 357
```

```
<210> SEQ ID NO 267
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.
```

```
<400> SEQUENCE: 267
gaggtgcagc tgttgagtc tggggaggc ttggtacagc ctggggggtc cctgcgctc 60
tcctgtgcag cctccgatt caccttttc aagtattcga tggggtgggt ccgccaggct 120
ccaggaagg gtctagagt ggtctcacag attcggata cgggtgatcg tagatactac 180
gatcactctg tgaagggcgc gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcggtggg aacctttgt ctactggggt caggaaccc tggtcaccgt ctcgagc 357
```

```
<210> SEQ ID NO 268
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.
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&lt;400&gt; SEQUENCE: 268

```

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt caccttttcc aagtattcga tgggggtgggt ccgccaggct   120
ccagggaaagg gtctagagtg ggtctcacag atttcggata cgggtgatcg tagatactac   180
gatgacgcgg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaggac accgcgggat attactgtgc gatataatcg   300
ggtcgttggg agccttttgt ctactggggg cagggaaacc tggtcaccgt ctcgagc   357

```

&lt;210&gt; SEQ ID NO 269

&lt;211&gt; LENGTH: 357

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 269

```

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt caccttttcc aagtattcga tgggggtgggt ccgccaggct   120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tagatactac   180
gatgactctg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaggac accgcgggat attactgtgc gatataatcg   300
ggtcgttggg agccttttgt ctactggggg cagggaaacc tggtcaccgt ctcgagc   357

```

&lt;210&gt; SEQ ID NO 270

&lt;211&gt; LENGTH: 357

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 270

```

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt caccttttcc aagtattcga tgggggtgggt ccgccaggct   120
ccagggaaagg gtctagagtg ggtctcacag atttcggata cgggtgatcg tagatactac   180
gatcactctg tgaagggccg gttcactatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaggac accgcgggat attactgtgc gatataatcg   300
ggtcgttggg agccttttgt ctactggggg cagggaaacc tggtcaccgt ctcgagc   357

```

&lt;210&gt; SEQ ID NO 271

&lt;211&gt; LENGTH: 357

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 271

```

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt caccttttcc aagtattcga tgggggtgggt ccgccaggct   120
ccagggaaagg gtctagagtg ggtctcacag atttcggata cgggtgatcg tagatactac   180
gatgacgcgg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaggac accgcgggat attactgtgc gatataatcg   300

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 ggtcgttggg agccttttgt ctactggggg cagggaaacc tggtcaccgt ctcgagc 357

<210> SEQ ID NO 272  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 272

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60  
 tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtggg cgcaggct 120  
 ccaggaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac 180  
 gcacactcog tgaagggcog gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240  
 ctgcaaatga acagcctgog tgccgaggac accgcggat attactgtgc gatatactac 300  
 ggtcgttggg agccttttgt ctactggggg cagggaaacc tggtcaccgt ctcgagc 357

<210> SEQ ID NO 273  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 273

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60  
 tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtggg cgcaggct 120  
 ccaggaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac 180  
 gcacactcog tgaagggcog gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240  
 ctgcaaatga acagcctgog tgccgaggac accgcggat attactgtgc gatatactac 300  
 ggtcgttggg tgccttttgc ctactggggg cagggaaacc tggtcaccgt ctcgagc 357

<210> SEQ ID NO 274  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 274

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60  
 tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtggg cgcaggct 120  
 ccaggaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac 180  
 gcacactcog tgaagggcog gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240  
 ctgcaaatga acagcctgog tgccgaggac accgcggat attactgtgc gatatactac 300  
 ggtcgttggg gaccttttca gtactggggg cagggaaacc tggtcaccgt ctcgagc 357

<210> SEQ ID NO 275  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 275

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

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tctctgtgcag cctccggatt cacctttggt aagtattcga tgggggtgggt ccgccaggct 120
ccaggggaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac 180
gcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcgttggg agccttttca gtactgggggt cagggaaactc tggtcaccgt ctcgagc 357

```

```

<210> SEQ ID NO 276
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 276

```

```

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tctctgtgcag cctccggatt cacctttggt aagtattcga tgggggtgggt ccgccaggct 120
ccaggggaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac 180
gcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcgttggg cgccttttga gtactgggggt cagggaaacc tggtcaccgt ctcgagc 357

```

```

<210> SEQ ID NO 277
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 277

```

```

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tctctgtgcag cctccggatt cacctttggt aagtattcga tgggggtgggt ccgccaggct 120
ccaggggaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac 180
gcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcgttggg cgccttttca gtactgggggt cagggaaactc tggtcaccgt ctcgagc 357

```

```

<210> SEQ ID NO 278
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 278

```

```

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tctctgtgcag cctccggatt cacctttggt aagtattcga tgggggtgggt ccgccaggct 120
ccaggggaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac 180
gcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcgttggg tgccttttca gtactgggggt cagggcacc tggtcaccgt ctcgagc 357

```

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<210> SEQ ID NO 279

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<211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 279

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tctctgtcag cctccgatt cacctttgt aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ccggtgatcg tagatactac	180
gatcactctg tgaagggccg gttcactatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac acccggtat attactgtgc gatataacg	300
ggtcggtggg cgccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 280  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 280

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tctctgtcag cctccgatt caccttttg aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac	180
gcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgctgaggac acccggtat attactgtgc gatataact	300
gggcgttggg tgccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 281  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 281

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tctctgtcag cctccgatt caccttttc aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac	180
gcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgctgaggac acccggtat attactgtgc gatataact	300
gggcgttggg tgccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc	357

<210> SEQ ID NO 282  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 282

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tctctgtcag cctccgatt caccttttg aagtattcga tgggggtgggt ccgccaggct	120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac	180

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gatcactcgc tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcgtttga ggccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc 357

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```

<210> SEQ ID NO 283
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 283

```

```

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt caccttttcc aagtattcga tgggggtgggt ccgccaggct 120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac 180
gatcactcgc tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcgtttga ggccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc 357

```

```

<210> SEQ ID NO 284
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 284

```

```

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt caccttttcc aagtattcga tgggggtgggt ccgccaggct 120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac 180
gatcactcgc tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcgtttggg agccttttgt ctactggggt cagggaaacc tggtcaccgt ctcgagc 357

```

```

<210> SEQ ID NO 285
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 285

```

```

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt caccttttcc aagtattcga tgggggtgggt ccgccaggct 120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac 180
gatcactcgc tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcgtttggg agccttttgt ctactggggt cagggaaacc tggtcaccgt ctcgagc 357

```

```

<210> SEQ ID NO 286
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:

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<223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 286

```

gaggtgcagc tgttgagtc tgggggagc ttggtacagc ctggggggc cctgcgtctc    60
tcctgtgcag cctccgatt caccttttg aagtattcga tgggggtggg cccagcagct    120
ccaggaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac    180
tcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat    240
ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gatatact    300
gggcgttggg tgccttttga gtactggggc caggaaccc tggtcaccgt ctcgagc    357

```

&lt;210&gt; SEQ ID NO 287

&lt;211&gt; LENGTH: 357

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 287

```

gaggtgcagc tgttgagtc tgggggagc ttggtacagc ctggggggc cctgcgtctc    60
tcctgtgcag cctccgatt caccttttc aagtattcga tgggggtggg cccagcagct    120
ccaggaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac    180
tcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat    240
ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gatatact    300
gggcgttggg tgccttttga gtactggggc caggaaccc tggtcaccgt ctcgagc    357

```

&lt;210&gt; SEQ ID NO 288

&lt;211&gt; LENGTH: 357

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 288

```

gaggtgcagc tgttgagtc tgggggagc ttggtacagc ctggggggc cctgcgtctc    60
tcctgtgcag cctccgatt caccttttc aagtattcga tgggggtggg cccagcagct    120
ccaggaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac    180
acacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat    240
ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gatatact    300
gggcgttggg tgccttttga gtactggggc caggaaccc tggtcaccgt ctcgagc    357

```

&lt;210&gt; SEQ ID NO 289

&lt;211&gt; LENGTH: 357

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 289

```

gaggtgcagc tgttgagtc tgggggagc ttggtacagc ctggggggc cctgcgtctc    60
tcctgtgcag cctccgatt caccttttg aagtattcga tgggggtggg cccagcagct    120
ccaggaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac    180
acacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat    240
ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gatatact    300

```

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gggcggttggg tgccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc 357

<210> SEQ ID NO 290  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 290

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttttc aagtattcga tgggggtgggt ccgccaggct 120

ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac 180

gcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300

ggtcggttggg cgccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc 357

<210> SEQ ID NO 291  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 291

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttttg aagtattcga tgggggtgggt ccgccaggct 120

ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac 180

gcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300

ggtcggttggg cgccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc 357

<210> SEQ ID NO 292  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 292

gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60

tcctgtgcag cctccggatt cacctttttg aagtattcga tgggggtgggt ccgccaggct 120

ccagggaaagg gtctagagtg ggtctcacag atttcggata ccggtgatcg tagatactac 180

gatcactctg tgaagggccg gttcactatc tcccgcgaca attccaagaa cacgctgtat 240

ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300

ggtcggttggg cgccttttga gtactggggt cagggaaacc tggtcaccgt ctcgagc 357

<210> SEQ ID NO 293  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 293

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```

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt caccttttcc aagtattcga tgggggtgggt ccgccaggct   120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ccggtgatcg tagatactac   180
gatcactctg tgaagggccg gttcactatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgcgaggac accgcggtat attactgtgc gatatactac   300
ggtcggtggg cgccttttga gtactggggg cagggaaacc tggtcaccgt ctcgagc     357

```

```

<210> SEQ ID NO 294
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 294

```

```

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct   120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac   180
gcacactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgcgc gatatactac   300
gggcgttggg tgccttttga gtactggggg cagggaaacc tggtcaccgt ctcgagc     357

```

```

<210> SEQ ID NO 295
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 295

```

```

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt cacctttttt aagtattcga tgggggtgggt ccgccaggct   120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac   180
gcacacgcgg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gatatactac   300
gggcgttggg tgccttttga gtactggggg cagggaaacc tggtcaccgt ctcgagc     357

```

```

<210> SEQ ID NO 296
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 296

```

```

gaggtgcagc tgttgagtc tgggggaggc ttggtgcagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt cacctttgtt aagtattcga tgggggtgggt ccgccaggct   120
ccagggaaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tacatactac   180
gatcactccg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gatatactac   300
gggcgttggg tgccttttga gtactggggg cagggaaacc tggtcaccgt ctcgagc     357

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<210> SEQ ID NO 297  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 297

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggggtggg cccaggct	120
ccaggaagg gtctagagt ggtctcacag attgcgata ctgctgatc tacatactac	180
gatcacgcgg tgaagggcgg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgctgaggac accgcggtat attactgtgc gatatact	300
gggcgttggg tgccttttga gtactggggc caggaacc tggtcaccgt ctgagc	357

<210> SEQ ID NO 298  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 298

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggggtggg cccaggct	120
ccaggaagg gtctagagt ggtctcacag attgcgata ctgctgatc tagatactac	180
gcacactcgg tgaagggcgg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatatactc	300
ggtcggtggg cgccttttga gtactggggc caggaacc tggtcaccgt ctgagc	357

<210> SEQ ID NO 299  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 299

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggggtggg cccaggct	120
ccaggaagg gtctagagt ggtctcacag atttccgata ctgctgatc tagatactac	180
gcacacgcgg tgaagggcgg gttcaccatc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatatactc	300
ggtcggtggg cgccttttga gtactggggc caggaacc tggtcaccgt ctgagc	357

<210> SEQ ID NO 300  
 <211> LENGTH: 357  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 300

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggggtggg cccaggct	120

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```

ccaggggaagg gtctagagtg ggtctcacag attgcggata ctgctgatcg tagatactac 180
gcacacgcgg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcggtggg cgccttttga gtactggggt caggggaacc ttggtcacctg ctcgagc 357

```

```

<210> SEQ ID NO 301
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 301

```

```

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggggtggg cccccaggct 120
ccaggggaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tagatactac 180
gatcacgcgg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcggtggg cgccttttga gtactggggt caggggaacc ttggtcacctg ctcgagc 357

```

```

<210> SEQ ID NO 302
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 302

```

```

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggggtggg cccccaggct 120
ccaggggaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tagatactac 180
gatcacgcgg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcggtggg cgccttttga gtactggggt caggggaacc ttggtcacctg ctcgagc 357

```

```

<210> SEQ ID NO 303
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 303

```

```

gaggtgcagc tggtggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccgatt cacctttgtt aagtattcga tgggggtggg cccccaggct 120
ccaggggaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tagatactac 180
gatcactcgg tgaagggccg gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gatataatcg 300
ggtcggtggg cgccttttga gtactggggt caggggaacc ttggtcacctg ctcgagc 357

```

```

<210> SEQ ID NO 304
<211> LENGTH: 357
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

```

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&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 304

```

gaggtgcagc tgctggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc      60
tcctgtgcag cctccggatt cacctttttc aagtattcga tgggggtgggt cgcgcaggct      120
ccaggggaagg gtctagagtg ggtctcacag atttcggata ctgctgatcg tagatactac      180
gatgacgcgg tgaagggcgg gttcaccatc acccgcgaca attccaagaa cacgctgtat      240
ctgcaaatga acagcctgcg tgccgaggac accgcgggat attactgtgc gatataatcg      300
ggtcgttggg agccttttgt ctactggggg caggggaacc tggtcaccgt ctcgagc      357

```

&lt;210&gt; SEQ ID NO 305

&lt;211&gt; LENGTH: 163

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 305

```

His Gly Glu Gly Thr Phe Thr Ser Asp Leu Ser Lys Gln Met Glu Glu
 1                               5                               10          15
Glu Ala Val Arg Leu Phe Ile Glu Trp Leu Lys Asn Gly Gly Pro Ser
 20                               25                               30
Ser Gly Ala Pro Pro Pro Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly
 35                               40                               45
Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
 50                               55                               60
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
 65                               70                               75                               80
Ser Gln Trp Ile Gly Ser Gln Leu Ser Trp Tyr Gln Gln Lys Pro Gly
 85                               90                               95
Lys Ala Pro Lys Leu Leu Ile Met Trp Arg Ser Ser Leu Gln Ser Gly
 100                              105                              110
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
 115                              120                              125
Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala
 130                              135                              140
Gln Gly Ala Ala Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu
 145                              150                              155                              160
Ile Lys Arg

```

&lt;210&gt; SEQ ID NO 306

&lt;211&gt; LENGTH: 489

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 306

```

catggtgaag gaacatttac cagtgacttg tcaaaacaga tggaagagga ggcagtgagg      60
ttatttattg agtggcttaa gaacggagga ccaagtagcg gggcacctcc gccatcgggt      120
ggtgaggcgg gttcaggcgg aggtggcagc ggcggtggcg ggtcggacat ccagatgacc      180
cagtctccat cctccctgtc tgcactctgta ggagaccgtg tcaccatcac ttgccgggca      240
agtcagtgga ttgggtctca gttatcttgg taccagcaga aaccagggaa agcccctaag      300

```

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```

ctcctgatca tgtggcgcttc ctcggtgcaa agtgggggtcc catcacgttt cagtggcagt 360
ggatctggga cagatttcac tctcaccatc agcagttctgc aacctgaaga ttttgctacg 420
tactactgtg ctcagggtgc ggcggtgcct aggacgttcg gccaaaggac caaggtggaa 480
atcaaacgg 489

```

```

<210> SEQ ID NO 307
<211> LENGTH: 163
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 307

```

```

His Gly Glu Gly Thr Phe Thr Ser Asp Leu Ser Lys Gln Met Glu Glu
 1           5           10          15
Glu Ala Val Arg Leu Phe Ile Glu Trp Leu Lys Asn Gly Gly Pro Ser
 20          25          30
Ser Gly Ala Pro Pro Pro Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly
 35          40          45
Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser
 50          55          60
Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala
 65          70          75          80
Ser Gln Trp Ile Gly Ser Gln Leu Ser Trp Tyr Gln Gln Lys Pro Gly
 85          90          95
Lys Ala Pro Lys Leu Leu Ile Met Trp Arg Ser Ser Leu Gln Ser Gly
100         105         110
Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu
115         120         125
Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala
130         135         140
Gln Gly Leu Arg His Pro Lys Thr Phe Gly Gln Gly Thr Lys Val Glu
145         150         155         160
Ile Lys Arg

```

```

<210> SEQ ID NO 308
<211> LENGTH: 489
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 308

```

```

catggtgaag gaacatttac cagtgacttg tcaaacaga tggaagagga ggcagtgcgg 60
ttatttattg agtggcctaa gaacggagga ccaagtagcg gggcacctcc gccatcgggt 120
ggtgaggcgg gttcaggcgg agtgggcagc ggcgggtggcg ggtcggacat ccagatgacc 180
cagtctccat cctccctgtc tgcattctga ggagaccgtg tcaccatcac ttgccgggca 240
agtcagtgga ttgggtctca gttatcttgg taccagcaga aaccagggaa agcccctaag 300
ctcctgatca tgtggcgcttc ctcggtgcaa agtgggggtcc catcacgttt cagtggcagt 360
ggatctggga cagatttcac tctcaccatc agcagttctgc aacctgaaga ttttgctacg 420
tactactgtg ctcagggttt gaggcacccct aagacgttcg gccaaaggac caaggtggaa 480
atcaaacgg 489

```

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<210> SEQ ID NO 309  
 <211> LENGTH: 163  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 309

His Gly Glu Gly Thr Phe Thr Ser Asp Leu Ser Lys Gln Met Glu Glu  
 1 5 10 15  
 Glu Ala Val Arg Leu Phe Ile Glu Trp Leu Lys Asn Gly Gly Pro Ser  
 20 25 30  
 Ser Gly Ala Pro Pro Pro Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly  
 35 40 45  
 Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser  
 50 55 60  
 Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala  
 65 70 75 80  
 Ser Gln Trp Ile Gly Ser Gln Leu Ser Trp Tyr Gln Gln Lys Pro Gly  
 85 90 95  
 Lys Ala Pro Lys Leu Leu Ile Met Trp Arg Ser Ser Leu Gln Ser Gly  
 100 105 110  
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu  
 115 120 125  
 Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala  
 130 135 140  
 Gln Gly Leu Met Lys Pro Met Thr Phe Gly Gln Gly Thr Lys Val Glu  
 145 150 155 160  
 Ile Lys Arg

<210> SEQ ID NO 310  
 <211> LENGTH: 489  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 310

catggtgaag gaacatttac cagtgacttg tcaaaacaga tggaagagga ggcagtgcgg 60  
 ttatttattg agtggcctaa gaacggagga ccaagtagcg gggcacctcc gccatcgggt 120  
 ggtggaggcg gttcaggcgg aggtggcagc ggcgggtggcg ggtcggacat ccagatgacc 180  
 cagtctccat cctccctgtc tgcattctgta ggagaccgtg tcaccatcac ttgccgggca 240  
 agtcagtgga ttgggtctca gttatcttgg taccagcaga aaccagggaa agcccctaag 300  
 ctctgatca tgtggcgctc ctcggtgcaa agtggggctc catcacgttt cagtggcagt 360  
 ggatctggga cagatttcac tctcaccatc agcagtctgc aacctgaaga ttttgctacg 420  
 tactactgtg ctcagggtct tatgaagcct atgacgttcg gccaaaggac caagtggtgaa 480  
 atcaaacgg 489

<210> SEQ ID NO 311  
 <211> LENGTH: 163  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 311

-continued

His Gly Glu Gly Thr Phe Thr Ser Asp Leu Ser Lys Gln Met Glu Glu  
 1 5 10 15  
 Glu Ala Val Arg Leu Phe Ile Glu Trp Leu Lys Asn Gly Gly Pro Ser  
 20 25 30  
 Ser Gly Ala Pro Pro Pro Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly  
 35 40 45  
 Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser  
 50 55 60  
 Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Ser Cys Arg Ala  
 65 70 75 80  
 Ser Gln Trp Ile Gly Ser Gln Leu Ser Trp Tyr Gln Gln Lys Pro Gly  
 85 90 95  
 Glu Ala Pro Lys Leu Leu Ile Met Trp Arg Ser Ser Leu Gln Ser Gly  
 100 105 110  
 Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu  
 115 120 125  
 Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala  
 130 135 140  
 Gln Gly Ala Ala Leu Pro Arg Thr Phe Gly Gln Gly Thr Lys Val Glu  
 145 150 155 160  
 Ile Lys Arg

<210> SEQ ID NO 312  
 <211> LENGTH: 489  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 312

```

catggtgaag gaacatttac cagtgacttg tcaaaacaga tggaagagga ggcagtgcgg      60
ttatttattg agtggcctaa gaacggagga ccaagtagcg gggcacctcc gccatcgggt      120
ggtgaggcgg gttcaggcgg aggtggcagc ggcggtgccg ggtcggacat ccagatgacc      180
cagtctccat cctccctgtc tgcattctgta ggagaccgtg tcaccatctc ttgccgggca      240
agtcagtgga ttgggtctca gttatcttgg taccagcaga aaccagggga agcccctaag      300
ctcctgatca tgtggcgctc ctcggtgcaa agtggggctc catcacgttt cagtggcagt      360
ggatctggga cagatttcac tctcaccatc agcagtctgc aacctgaaga ttttgctacg      420
tactactgtg ctcagggtgc ggcggtgcct aggacgttcg gccaaaggac caaggtggaa      480
atcaaacgg                                     489
  
```

<210> SEQ ID NO 313  
 <211> LENGTH: 163  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 313

His Gly Glu Gly Thr Phe Thr Ser Asp Leu Ser Lys Gln Met Glu Glu  
 1 5 10 15  
 Glu Ala Val Arg Leu Phe Ile Glu Trp Leu Lys Asn Gly Gly Pro Ser  
 20 25 30  
 Ser Gly Ala Pro Pro Pro Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly  
 35 40 45

-continued

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Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser  
 50 55 60

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala  
 65 70 75 80

Ser Arg Pro Ile Gly Thr Thr Leu Ser Trp Tyr Gln Gln Lys Pro Gly  
 85 90 95

Lys Ala Pro Lys Leu Leu Ile Trp Phe Gly Ser Arg Leu Gln Ser Gly  
 100 105 110

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu  
 115 120 125

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala  
 130 135 140

Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly Thr Lys Val Glu  
 145 150 155 160

Ile Lys Arg

<210> SEQ ID NO 314  
 <211> LENGTH: 489  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 314

```

catggtgaag gaacatttac cagtgacttg tcaaaacaga tggaagagga ggcagtgcgg      60
ttatttattg agtggcctaa gaacggagga ccaagtagcg gggcacctcc gccatcgggt      120
ggtgaggcgg gttcaggcgg aggtggcagc ggcggtgccg ggtcggacat ccagatgacc      180
cagtctccat cctccctgtc tgcattctgta ggagaccgtg tcaccatcac ttgccgggca      240
agtcgtccga ttgggacgac gttaagttgg taccagcaga aaccagggaa agcccctaag      300
ctcctgatct ggtttggttc ccggttgcaa agtgggggtcc catcacgttt cagtggcagt      360
ggatctggga cagatttcac tctcaccatc agcagtctgc aacctgaaga ttttgctacg      420
tactactgtg cgcaggctgg gacgcatact acgacgttcg gccaaaggac caaggtggaa      480
atcaaacgg                                     489

```

<210> SEQ ID NO 315  
 <211> LENGTH: 163  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 315

His Gly Glu Gly Thr Phe Thr Ser Asp Leu Ser Lys Gln Met Glu Glu  
 1 5 10 15

Glu Ala Val Arg Leu Phe Ile Glu Trp Leu Lys Asn Gly Gly Pro Ser  
 20 25 30

Ser Gly Ala Pro Pro Pro Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly  
 35 40 45

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser  
 50 55 60

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala  
 65 70 75 80

Ser Arg Pro Ile Gly Thr Met Leu Ser Trp Tyr Gln Gln Lys Pro Gly  
 85 90 95

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Lys Ala Pro Lys Leu Leu Ile Leu Phe Gly Ser Arg Leu Gln Ser Gly  
 100 105 110

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu  
 115 120 125

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala  
 130 135 140

Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly Thr Lys Val Glu  
 145 150 155 160

Ile Lys Arg

<210> SEQ ID NO 316  
 <211> LENGTH: 489  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 316

```

catggtgaag gaacatttac cagtgacttg tcaaaacaga tggaagagga ggcagtgcgg      60
ttatttattg agtggcctaa gaacggagga ccaagtagcg gggcacctcc gccatcgggt      120
ggtgaggcgg gttcaggcgg agtgggcagc ggcggtgggc ggteggacat ccagatgacc      180
cagtctccat cctccctgtc tgcactctga ggagaccgtg tcaccatcac ttgccgggca      240
agtcgtccga ttgggacgat gttaagttgg taccagcaga aaccagggaa agcccctaag      300
ctcctgatct tgtttggttc ccggttgcaa agtgggggtcc catcacgttt cagtggcagt      360
ggatctggga cagatttcac tctcaccatc agcagtctgc aacctgaaga ttttgctacg      420
tactactgtg cgcaggctgg gacgcatact acgacgttcg gccaaaggac caaggtggaa      480
atcaaacgg                                     489

```

<210> SEQ ID NO 317  
 <211> LENGTH: 163  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 317

His Gly Glu Gly Thr Phe Thr Ser Asp Leu Ser Lys Gln Met Glu Glu  
 1 5 10 15

Glu Ala Val Arg Leu Phe Ile Glu Trp Leu Lys Asn Gly Gly Pro Ser  
 20 25 30

Ser Gly Ala Pro Pro Pro Ser Gly Gly Gly Gly Gly Ser Gly Gly Gly  
 35 40 45

Gly Ser Gly Gly Gly Gly Ser Asp Ile Gln Met Thr Gln Ser Pro Ser  
 50 55 60

Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr Cys Arg Ala  
 65 70 75 80

Ser Arg Pro Ile Gly Thr Met Leu Ser Trp Tyr Gln Gln Lys Pro Gly  
 85 90 95

Lys Ala Pro Lys Leu Leu Ile Leu Ala Phe Ser Arg Leu Gln Ser Gly  
 100 105 110

Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu  
 115 120 125

Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Ala  
 130 135 140

-continued

Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly Thr Lys Val Glu  
145 150 155 160

Ile Lys Arg

<210> SEQ ID NO 318  
<211> LENGTH: 489  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 318

```
catggtgaag gaacatttac cagtgacttg tcaaaacaga tggaagagga ggcagtgcgg      60
ttatttattg agtggcctaa gaacggagga ccaagtagcg gggcacctcc gccatcgggt      120
ggtggaggcg gttcaggcgg aggtggcagc ggcggtggcg ggtcggacat ccagatgacc      180
cagtctccat cctccctgtc tgcattctga ggagaccgtg tcaccatcac ttgccgggca      240
agtctgccga ttgggacgat gttaagttgg taccagcaga aaccagggaa agcccctaag      300
ctcctgatcc ttgcttttcc cgttttgcaa agtggggctc catcacgttt cagtggcagt      360
ggatctggga cagatttcac tctcaccatc agcagtctgc aacctgaaga tttgctacg      420
tactactcgc cgcaggctgg gacgcatact acgacgttcg gccaaaggac caagtgga      480
atcaaacgg                                     489
```

<210> SEQ ID NO 319  
<211> LENGTH: 114  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 319

```
Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
  1           5           10           15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Trp Ile Gly Ser Gln
          20           25           30
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35           40           45
Met Trp Arg Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
          50           55           60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
          65           70           75           80
Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Gly Leu Arg His Pro Lys
          85           90           95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Gly Gly Gly Gly
          100          105          110
```

Ser Cys

<210> SEQ ID NO 320  
<211> LENGTH: 345  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 320

```
gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc      60
ataccttgcc gggcaagtca gtggattggg tctcagttat cttggtacca gcagaaacca      120
```

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```

gggaaagccc ctaagctcct gatcatgtgg cgttcctcgt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtgatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgctcag ggtttgagggc atcctaagac gttcggccaa 300
gggaccaagg tggaaatcaa acgggggtgc ggagggggtt cctgt 345

```

```

<210> SEQ ID NO 321
<211> LENGTH: 115
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 321

```

```

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1           5           10          15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Trp Ile Gly Ser Gln
          20          25          30
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
          35          40          45
Met Trp Arg Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
          50          55          60
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65          70          75          80
Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Gly Leu Arg His Pro Lys
          85          90          95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala
          100         105         110
Pro Ser Cys
          115

```

```

<210> SEQ ID NO 322
<211> LENGTH: 345
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 322

```

```

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc 60
atcaactgccc gggcaagtca gtggattggg tctcagttat cttggtacca gcagaaacca 120
gggaaagccc ctaagctcct gatcatgtgg cgttcctcgt tgcaaagtgg ggtcccatca 180
cgtttcagtg gcagtgatc tgggacagat ttcactctca ccatcagcag tctgcaacct 240
gaagattttg ctacgtacta ctgtgctcag ggtttgagggc atcctaagac gttcggccaa 300
gggaccaagg tggaaatcaa acggaccgtc gctgctccat cttgt 345

```

```

<210> SEQ ID NO 323
<211> LENGTH: 235
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 323

```

```

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1           5           10          15
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Arg Tyr

```

-continued

20					25					30					
Ser	Met	Gly	Trp	Leu	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
	35					40					45				
Ser	Arg	Ile	Asp	Ser	Tyr	Gly	Arg	Gly	Thr	Tyr	Tyr	Glu	Asp	Pro	Val
	50					55					60				
Lys	Gly	Arg	Phe	Ser	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
	65					70					75				80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Lys	Ile	Ser	Gln	Phe	Gly	Ser	Asn	Ala	Phe	Asp	Tyr	Trp	Gly	Gln
			100						105					110	
Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Ser	Gly	Pro	Ser	Asp
			115					120					125		
Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp
	130					135					140				
Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Arg	Pro	Ile	Gly	Thr	Thr	Leu
	145					150					155				160
Ser	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	Ile	Trp
				165					170					175	
Phe	Gly	Ser	Arg	Leu	Gln	Ser	Gly	Val	Pro	Ser	Arg	Phe	Ser	Gly	Ser
			180						185					190	
Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	Leu	Gln	Pro	Glu
			195					200					205		
Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Ala	Gln	Ala	Gly	Thr	His	Pro	Thr	Thr
	210					215					220				
Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	Arg					
	225					230					235				

&lt;210&gt; SEQ ID NO 324

&lt;211&gt; LENGTH: 249

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 324

Glu	Val	Gln	Leu	Leu	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly
	1			5					10					15	
Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Asn	Arg	Tyr
			20						25					30	
Ser	Met	Gly	Trp	Leu	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val
		35					40					45			
Ser	Arg	Ile	Asp	Ser	Tyr	Gly	Arg	Gly	Thr	Tyr	Tyr	Glu	Asp	Pro	Val
	50					55					60				
Lys	Gly	Arg	Phe	Ser	Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr
	65					70					75				80
Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	
Ala	Lys	Ile	Ser	Gln	Phe	Gly	Ser	Asn	Ala	Phe	Asp	Tyr	Trp	Gly	Gln
			100						105					110	
Gly	Thr	Gln	Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Ser	Gly	Pro	Ser	Asp
			115					120					125		
Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp
	130					135					140				
Arg	Val	Thr	Ile	Thr	Cys	Arg	Ala	Ser	Arg	Pro	Ile	Gly	Thr	Thr	Leu

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145	150	155	160
Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Trp	165	170	175
Phe Gly Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser	180	185	190
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu	195	200	205
Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr Thr	210	215	220
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Glu Gln	225	230	235
Lys Leu Ile Ser Glu Asp Leu Asn	245		

<210> SEQ ID NO 325  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 325

```

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccgatt cacctttaat aggtatagta tgggggtggct ccgccaggct   120
ccagggaaag gtctagagtg ggtctcacgg attgattctt atggtcgtgg tacatactac   180
gaagaccccg tgaagggccg gttcagcadc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaggac accgccgtat attactgtgc gaaaatttct   300
cagtttgggt caaatgcggt tgactactgg ggtcagggaa cccaggtcac cgtctcgagc   360
gctagcacca gtggtccatc ggacatccag atgacccagt ctccatcctc cctgtctgca   420
tctgtaggag accgtgtcac catcacttgc cgggcaagtc gtccgattgg gacgacgtta   480
agttggtaac agcagaaacc agggaaagcc cctaagctcc tgatctgggt tggttcccgg   540
ttgcaaagtg ggggtccatc acgtttcagt ggcagtggat ctgggacaga ttctactctc   600
accatcagca gtctgcaacc tgaagatctt gctacgtact actgtgcgca ggctgggacg   660
catctacgca cgttcggcca agggaccaag gtggaatca aacgg                               705

```

<210> SEQ ID NO 326  
 <211> LENGTH: 750  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 326

```

gaggtgcagc tgttgagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccgatt cacctttaat aggtatagta tgggggtggct ccgccaggct   120
ccagggaaag gtctagagtg ggtctcacgg attgattctt atggtcgtgg tacatactac   180
gaagaccccg tgaagggccg gttcagcadc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaggac accgccgtat attactgtgc gaaaatttct   300
cagtttgggt caaatgcggt tgactactgg ggtcagggaa cccaggtcac cgtctcgagc   360
gctagcacca gtggtccatc ggacatccag atgacccagt ctccatcctc cctgtctgca   420
tctgtaggag accgtgtcac catcacttgc cgggcaagtc gtccgattgg gacgacgtta   480

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```

agttggtacc agcagaaacc agggaaagcc cctaagctcc tgatctggtt tggttcccgg 540
ttgcaaagtg gggteccatc acgtttcagt ggcagtgat ctgggacaga tttcaactctc 600
accatcagca gtctgcaacc tgaagatddd gctacgtact actgtgcgca ggctgggacg 660
catcctacga cgttcggcca agggaccaag gtggaaatca aacgggcccgc cgcagaacaa 720
aaactcatct cagaagagga tctgaattaa 750

```

```

<210> SEQ ID NO 327
<211> LENGTH: 235
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 327

```

```

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1          5          10
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Arg Tyr
 20          25          30
Ser Met Gly Trp Leu Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35          40          45
Ser Arg Ile Asp Ser Tyr Gly Arg Gly Thr Tyr Tyr Glu Asp Pro Val
 50          55          60
Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
 65          70          75
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
 85          90          95
Ala Lys Ile Ser Gln Phe Gly Ser Asn Ala Phe Asp Tyr Trp Gly Gln
 100          105          110
Gly Thr Gln Val Thr Val Ser Ser Ala Ser Thr Ser Gly Pro Ser Asp
 115          120          125
Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp
 130          135          140
Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met Leu
 145          150          155
Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Leu
 165          170          175
Phe Gly Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser
 180          185          190
Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu
 195          200          205
Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr Thr
 210          215          220
Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
 225          230          235

```

```

<210> SEQ ID NO 328
<211> LENGTH: 249
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 328

```

```

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly
 1          5          10          15

```



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---

<210> SEQ ID NO 330  
 <211> LENGTH: 750  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 330

gaggtgcagc tgttgagtc tgggggagc ttggtacagc ctggggggtc cctgcgtctc	60
tcctgtgcag cctccggatt caccttaat aggtatagta tgggggtggct ccgccaggct	120
ccagggaagg gtctagagtg ggtctcacgg attgattctt atggctcgtgg tacatactac	180
gaagaccccg tgaagggcgc gttcagcadc tcccgcgaca attccaagaa cacgctgtat	240
ctgcaaatga acagcctgcg tgccgaggac accgccgtat attactgtgc gaaaatttct	300
cagtttgggt caaatgcgct tgactactgg ggtcagggaa cccaggtcac cgtctcgagc	360
gctagcacca gtggtccatc ggacatccag atgaccocag ctccatcctc cctgtctgca	420
tctgtaggag accgtgtcac catcacttgc cgggcaagtc gtccgattgg gacgatgta	480
agttgggtacc agcagaaaacc agggaaagcc cctaagctcc tgatcttgtt tggttcccg	540
ttgcaaagtg gggctccatc acgtttcagt ggcagtgat ctgggacaga tttcactctc	600
accatcagca gtctgcaacc tgaagatttt gctacgtact actgtgcgca ggctgggacg	660
catcctacga cgttccgcca agggaccaag gtggaatca aacgggcggc cgcagaacaa	720
aaactcatct cagaagagga tctgaattaa	750

<210> SEQ ID NO 331  
 <211> LENGTH: 235  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 331

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly	
1 5 10 15	
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Arg Tyr	
20 25 30	
Ser Met Gly Trp Leu Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val	
35 40 45	
Ser Arg Ile Asp Ser Tyr Gly Arg Gly Thr Tyr Tyr Glu Asp Pro Val	
50 55 60	
Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr	
65 70 75 80	
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys	
85 90 95	
Ala Lys Ile Ser Gln Phe Gly Ser Asn Ala Phe Asp Tyr Trp Gly Gln	
100 105 110	
Gly Thr Gln Val Thr Val Ser Ser Ala Ser Thr Ser Gly Pro Ser Asp	
115 120 125	
Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp	
130 135 140	
Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met Leu	
145 150 155 160	
Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Leu	
165 170 175	

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Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser  
 180 185 190

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu  
 195 200 205

Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr Thr  
 210 215 220

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg  
 225 230 235

<210> SEQ ID NO 332  
 <211> LENGTH: 249  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 332

Glu Val Gln Leu Leu Glu Ser Gly Gly Gly Leu Val Gln Pro Gly Gly  
 1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Asn Arg Tyr  
 20 25 30

Ser Met Gly Trp Leu Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val  
 35 40 45

Ser Arg Ile Asp Ser Tyr Gly Arg Gly Thr Tyr Tyr Glu Asp Pro Val  
 50 55 60

Lys Gly Arg Phe Ser Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr  
 65 70 75 80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys  
 85 90 95

Ala Lys Ile Ser Gln Phe Gly Ser Asn Ala Phe Asp Tyr Trp Gly Gln  
 100 105 110

Gly Thr Gln Val Thr Val Ser Ser Ala Ser Thr Ser Gly Pro Ser Asp  
 115 120 125

Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp  
 130 135 140

Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met Leu  
 145 150 155 160

Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Leu  
 165 170 175

Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser  
 180 185 190

Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu  
 195 200 205

Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr Thr  
 210 215 220

Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Glu Gln  
 225 230 235 240

Lys Leu Ile Ser Glu Glu Asp Leu Asn  
 245

<210> SEQ ID NO 333  
 <211> LENGTH: 705  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 333

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gaggtgcagc tgttgagtc tgggggagc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt cacctttaat aggtatagta tgggggtggt ccgccaggct   120
ccaggaagg gtctagagtg ggtctcacgg attgattctt atggctgtgg tacatactac   180
gaagaccccg tgaagggcgc gttcagcadc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaggac accgcogtat attactgtgc gaaaatttct   300
cagtttgggt caaatgcggt tgactactgg ggtcagggaa cccaggtcac cgtctcgagc   360
gctagcacca gtggtccatc ggacatccag atgaccagc ctccatcctc cctgtctgca   420
tctgtaggag accgtgtcac catcacttgc cgggcaagtc gtccgattgg gacgatgta   480
agttggtacc agcagaaaacc agggaaagcc cctaagctcc tgatccttgc tttttcccgt   540
tgcaaaagtg gggcccacac acgtttcagt ggcagtggat ctgggacaga tttaactctc   600
accatcagca gtctgcaacc tgaagatatt gctacgtact actgocgca ggctgggacg   660
catcctacga cgttcggcca agggaccaag gtggaatca aacgg                               705

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<210> SEQ ID NO 334
<211> LENGTH: 750
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 334

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gaggtgcagc tgttgagtc tgggggagc ttggtacagc ctggggggtc cctgcgtctc   60
tcctgtgcag cctccggatt cacctttaat aggtatagta tgggggtggt ccgccaggct   120
ccaggaagg gtctagagtg ggtctcacgg attgattctt atggctgtgg tacatactac   180
gaagaccccg tgaagggcgc gttcagcadc tcccgcgaca attccaagaa cacgctgtat   240
ctgcaaatga acagcctgcg tgccgaggac accgcogtat attactgtgc gaaaatttct   300
cagtttgggt caaatgcggt tgactactgg ggtcagggaa cccaggtcac cgtctcgagc   360
gctagcacca gtggtccatc ggacatccag atgaccagc ctccatcctc cctgtctgca   420
tctgtaggag accgtgtcac catcacttgc cgggcaagtc gtccgattgg gacgatgta   480
agttggtacc agcagaaaacc agggaaagcc cctaagctcc tgatccttgc tttttcccgt   540
tgcaaaagtg gggcccacac acgtttcagt ggcagtggat ctgggacaga tttaactctc   600
accatcagca gtctgcaacc tgaagatatt gctacgtact actgocgca ggctgggacg   660
catcctacga cgttcggcca agggaccaag gtggaatca aacggggcgc cgcagaacaa   720
aaactcatct cagaagagga tctgaattaa                               750

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<210> SEQ ID NO 335
<211> LENGTH: 9
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 335

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Ser Gln Ser Ile Ser Ser Tyr Leu Asn
 1                               5

```

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<210> SEQ ID NO 336
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Homo Sapiens

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<400> SEQUENCE: 336

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Tyr Ala Ala Ser Ser Leu Gln Ser  
1 5

<210> SEQ ID NO 337  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 337

Gln Gln Ser Tyr Ser Thr Pro Asn Thr  
1 5

<210> SEQ ID NO 338  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 338

Ser Arg Pro Ile Gly Thr Thr Leu Ser  
1 5

<210> SEQ ID NO 339  
<211> LENGTH: 8  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 339

Trp Phe Gly Ser Arg Leu Gln Ser  
1 5

<210> SEQ ID NO 340  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 340

Ala Gln Ala Gly Thr His Pro Thr Thr  
1 5

<210> SEQ ID NO 341  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 341

Ser Arg Pro Ile Gly Thr Met Leu Ser  
1 5

<210> SEQ ID NO 342  
<211> LENGTH: 8  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 342

Leu Phe Gly Ser Arg Leu Gln Ser  
1 5

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<210> SEQ ID NO 343  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 343

Ala Gln Ala Gly Thr His Pro Thr Thr  
1 5

<210> SEQ ID NO 344  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 344

Ser Arg Pro Ile Gly Thr Met Leu Ser  
1 5

<210> SEQ ID NO 345  
<211> LENGTH: 8  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 345

Leu Ala Phe Ser Arg Leu Gln Ser  
1 5

<210> SEQ ID NO 346  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 346

Ala Gln Ala Gly Thr His Pro Thr Thr  
1 5

<210> SEQ ID NO 347  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 347

Ser Arg Pro Ile Gly Thr Met Leu Ser  
1 5

<210> SEQ ID NO 348  
<211> LENGTH: 8  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 348

Trp Phe Gly Ser Arg Leu Gln Ser  
1 5

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<210> SEQ ID NO 349  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 349

Ala Gln Ala Gly Thr His Pro Thr Thr  
1 5

<210> SEQ ID NO 350  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 350

Ser Arg Pro Ile Gly Thr Met Leu Ser  
1 5

<210> SEQ ID NO 351  
<211> LENGTH: 8  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 351

Leu Phe Gly Ser Arg Leu Gln Ser  
1 5

<210> SEQ ID NO 352  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 352

Ala Gln Thr Gly Thr His Pro Thr Thr  
1 5

<210> SEQ ID NO 353  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 353

Ser Arg Pro Ile Gly Thr Thr Leu Ser  
1 5

<210> SEQ ID NO 354  
<211> LENGTH: 8  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 354

Leu Trp Phe Ser Arg Leu Gln Ser  
1 5

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<210> SEQ ID NO 355  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 355

Ala Gln Ala Gly Thr His Pro Thr Thr  
1 5

<210> SEQ ID NO 356  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 356

Ser Gln Trp Ile Gly Ser Gln Leu Ser  
1 5

<210> SEQ ID NO 357  
<211> LENGTH: 8  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 357

Met Trp Arg Ser Ser Leu Gln Ser  
1 5

<210> SEQ ID NO 358  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 358

Ala Gln Gly Ala Ala Leu Pro Arg Thr  
1 5

<210> SEQ ID NO 359  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 359

Ser Gln Trp Ile Gly Ser Gln Leu Ser  
1 5

<210> SEQ ID NO 360  
<211> LENGTH: 8  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 360

Met Trp Arg Ser Ser Leu Gln Ser  
1 5

<210> SEQ ID NO 361

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<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 361

Ala Gln Gly Leu Arg His Pro Lys Thr  
1 5

<210> SEQ ID NO 362  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 362

Ser Gln Trp Ile Gly Ser Gln Leu Ser  
1 5

<210> SEQ ID NO 363  
<211> LENGTH: 8  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 363

Met Trp Arg Ser Ser Leu Gln Ser  
1 5

<210> SEQ ID NO 364  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 364

Ala Gln Gly Leu Met Lys Pro Met Thr  
1 5

<210> SEQ ID NO 365  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 365

Ser Gln Trp Ile Gly Ser Gln Leu Ser  
1 5

<210> SEQ ID NO 366  
<211> LENGTH: 8  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 366

Met Trp Arg Ser Ser Leu Gln Ser  
1 5

<210> SEQ ID NO 367  
<211> LENGTH: 9

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<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 367

Ala Gln Gly Ala Ala Leu Pro Arg Thr  
1 5

<210> SEQ ID NO 368  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 368

Ser Gln Trp Ile Gly Ser Gln Leu Ser  
1 5

<210> SEQ ID NO 369  
<211> LENGTH: 8  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 369

Met Trp Arg Ser Ser Leu Gln Ser  
1 5

<210> SEQ ID NO 370  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 370

Ala Gln Gly Ala Ala Leu Pro Lys Thr  
1 5

<210> SEQ ID NO 371  
<211> LENGTH: 9  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 371

Ser Gln Trp Ile Gly Ser Gln Leu Ser  
1 5

<210> SEQ ID NO 372  
<211> LENGTH: 8  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 372

Met Trp Arg Ser Ser Leu Gln Ser  
1 5

<210> SEQ ID NO 373  
<211> LENGTH: 9  
<212> TYPE: PRT

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<213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 373

Ala Gln Gly Phe Lys Lys Pro Arg Thr  
 1 5

<210> SEQ ID NO 374  
 <211> LENGTH: 165  
 <212> TYPE: PRT  
 <213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 374

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met  
 1 5 10 15  
 Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp  
 20 25 30  
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln  
 35 40 45  
 Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe  
 50 55 60  
 Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu  
 65 70 75 80  
 Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu  
 85 90 95  
 Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys  
 100 105 110  
 Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu  
 115 120 125  
 Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg  
 130 135 140  
 Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser  
 145 150 155 160  
 Leu Arg Ser Lys Glu  
 165

<210> SEQ ID NO 375  
 <211> LENGTH: 495  
 <212> TYPE: DNA  
 <213> ORGANISM: Homo Sapiens

<400> SEQUENCE: 375

tgtgatctgc ctcaaaccca cagcctgggt agcaggagga ccttgatgct cctggcacag 60  
 atgaggagaa tctctctttt ctctgcttg aaggacagac atgactttgg atttcccag 120  
 gaggagtgtt gcaaccagtt ccaaaaaggct gaaaccatcc ctgtcctcca tgagatgatc 180  
 cagcagatct tcaatctctt cagcacaaaag gactcatctg ctgcttggga tgagaccctc 240  
 ctagacaaat tctacactga actctaccag cagctgaatg acctggaagc ctgtgtgata 300  
 cagggggtgg ggggtacaga gactcccctg atgaaggagg actccattct ggctgtgagg 360  
 aaatacttcc aaagaatcac tctctatctg aaagagaaga aatacagccc ttgtgcctgg 420  
 gaggttgta gagcagaat catgagatct tttctttgt caacaaactt gcaagaaagt 480  
 ttaagaagta aggaa 495

<210> SEQ ID NO 376  
 <211> LENGTH: 25

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<212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.  
 <400> SEQUENCE: 376  
 gcccgatcc accggtgtg atctg 25

<210> SEQ ID NO 377  
 <211> LENGTH: 30  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.  
 <400> SEQUENCE: 377  
 ggagatgga gactgggtca tctggatgc 30

<210> SEQ ID NO 378  
 <211> LENGTH: 30  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.  
 <400> SEQUENCE: 378  
 gacatccaga tgaccagtc tccatctcc 30

<210> SEQ ID NO 379  
 <211> LENGTH: 82  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.  
 <400> SEQUENCE: 379  
 ggcgaagctt ttattaattc agatcctctt ctgagatgag ttttgttct gcggccgcc 60  
 gtttgatttc caccttggtc cc 82

<210> SEQ ID NO 380  
 <211> LENGTH: 56  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.  
 <400> SEQUENCE: 380  
 gcccgatcc accggtgtg atctggcgca agcttttatt aatcagatc ctcttc 56

<210> SEQ ID NO 381  
 <211> LENGTH: 51  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.  
 <400> SEQUENCE: 381  
 tgagatgagt ttttgtctg cggccgccg tttgatttcc accttgggtc c 51

<210> SEQ ID NO 382  
 <211> LENGTH: 1  
 <212> TYPE: PRT  
 <213> ORGANISM: Murine  
 <400> SEQUENCE: 382

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Gly  
1

<210> SEQ ID NO 383  
 <211> LENGTH: 61  
 <212> TYPE: DNA  
 <213> ORGANISM: Murine

&lt;400&gt; SEQUENCE: 383

atggagaccg acaccctgct gctgtgggtg ctgctgctgt gggtgcccgg atccaccggg 60

c 61

<210> SEQ ID NO 384  
 <211> LENGTH: 293  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 384

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met  
1 5 10 15Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp  
20 25 30Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln  
35 40 45Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe  
50 55 60Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu  
65 70 75 80Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu  
85 90 95Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys  
100 105 110Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu  
115 120 125Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg  
130 135 140Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser  
145 150 155 160Leu Arg Ser Lys Glu Thr Val Ala Ala Pro Ser Asp Ile Gln Met Thr  
165 170 175Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile  
180 185 190Thr Cys Arg Ala Ser Gln Trp Ile Gly Ser Gln Leu Ser Trp Tyr Gln  
195 200 205Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Met Trp Arg Ser Ser  
210 215 220Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr  
225 230 235 240Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr  
245 250 255Tyr Tyr Cys Ala Gln Gly Ala Ala Leu Pro Arg Thr Phe Gly Gln Gly  
260 265 270Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Glu Gln Lys Leu Ile Ser  
275 280 285

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Glu Glu Asp Leu Asn  
290

<210> SEQ ID NO 385  
<211> LENGTH: 882  
<212> TYPE: DNA  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 385

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tgcgacttgc cacagacaca tagtttggga tcaagaagaa cattgatggt attagcacia    60
atgcgtagaa tttctttggt ctcttgtcta aaggaccgtc acgacttcgg attccctcag    120
gaagagtttg gaaaccaatt ccaaaaagca gaaactattc ctgtcttgca cgaatgatc    180
cagcaaatat tcaatttgtt ttctacaaag gactcatcag ccgcttggga tgaactctg    240
ttagataaat tctacactga actatatcaa caactgaacg atctagaggc ttgcgttatt    300
caggggttag gagttactga aactccccta atgaaagaag attcaattct agccgttaga    360
aaatactttc agcgtatcac attgtattta aaggaaaaga aatactcccc atgtgcatgg    420
gaggtgggta gagcagaaat tatgaggtcc ttctctcttt ctacgaattt gcaagaatct    480
ttgagatcta aggaaaccgt cgctgtccca tctgacatcc agatgaccca gtctccatcc    540
tccctgtctg catctgtagg agaccgtgtc accatcaett gccgggcaag tcagtggatt    600
gggtctcagt tatcttggtg ccagcagaaa ccagggaag cccctaagct cctgatcatg    660
tggcgttcct cgttgcaaag tggggtocca tcacgtttca gtggcagtgg atctgggaca    720
gatttcactc tcaccatcag cagtctgcaa cctgaagatt ttgctacgta ctactgtgct    780
cagggtgctg cgttgcctag gacgttcggc caagggacca aggtggaat caaacgggctg    840
gccgcagaac aaaaactcat ctcaagaag gatctgaatt aa                        882

```

<210> SEQ ID NO 386  
<211> LENGTH: 279  
<212> TYPE: PRT  
<213> ORGANISM: Artificial Sequence  
<220> FEATURE:  
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 386

```

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
 1           5           10           15
Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
 20           25           30
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
 35           40           45
Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
 50           55           60
Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
 65           70           75           80
Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
 85           90           95
Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
 100          105          110
Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
 115          120          125
Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
 130          135          140

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Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser  
 145 150 155 160  
 Leu Arg Ser Lys Glu Thr Val Ala Ala Pro Ser Asp Ile Gln Met Thr  
 165 170 175  
 Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile  
 180 185 190  
 Thr Cys Arg Ala Ser Gln Trp Ile Gly Ser Gln Leu Ser Trp Tyr Gln  
 195 200 205  
 Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Met Trp Arg Ser Ser  
 210 215 220  
 Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr  
 225 230 235 240  
 Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr  
 245 250 255  
 Tyr Tyr Cys Ala Gln Gly Ala Ala Leu Pro Arg Thr Phe Gly Gln Gly  
 260 265 270  
 Thr Lys Val Glu Ile Lys Arg  
 275

<210> SEQ ID NO 387  
 <211> LENGTH: 837  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 387

tgcgacttgc cacagacaca tagtttggga tcaagaagaa cattgatggt attagcacia 60  
 atgcgtagaa tttctttggt ctcttgctca aaggaccgtc acgacttcgg attccctcag 120  
 gaagagtttg gaaaccaatt ccaaaaagca gaaactattc ctgtcttgca cgaaatgatc 180  
 cagcaaatat tcaatttgtt ttctacaaag gactcatcag ccgcttggga tgaactctg 240  
 ttagataaat tctacactga actatatcaa caactgaacg atctagaggg ttgcgttatt 300  
 cagggtgtag gagttactga aactccccta atgaaagaag attcaattct agccgtaga 360  
 aaatactttc agcgtatcac attgtattta aaggaaaaga aatactcccc atgtgcatgg 420  
 gaggtgggta gagcagaaat tatgaggtcc ttctctcttt ctacgaattt gcaagaatct 480  
 ttgagatcta aggaaaccgt cgctgctcca tctgacatcc agatgaccca gtctccatcc 540  
 tccctgtctg catctgtagg agaccgtgtc accatcactt gccgggcaag tcagtggtatt 600  
 gggctctcagt tatcttggtg ccagcagaaa ccagggaaag ccctaagct cctgatcatg 660  
 tggcgttcct cgttgcaaag tggggtocca tcacgtttca gtggcagtg atctgggaca 720  
 gatttcactc tcaccatcag cagtctgcaa cctgaagatt ttgctacgta ctactgtgct 780  
 cagggtgcgg cgttgcctag gacgttcggc caagggacca aggtggaat caaacgg 837

<210> SEQ ID NO 388  
 <211> LENGTH: 293  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 388

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met  
 1 5 10 15



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ttgagatcta aggaaaccgt cgctgctcca tctgacatcc agatgaccca gtctccatcc 540
tccctgtctg catctgtagg agaccgtgtc accatcactt gccgggcaag tcagtggatt 600
gggtctcagt tatcttgta ccagcagaaa ccagggaag cccctaagct cctgatcatg 660
tggcgttcct cgttgcaaag tggggtocca tcacgtttca gtggcagtgg atctgggaca 720
gatttcactc tcaccatcag cagtctgcaa cctgaagatt ttgctacgta ctactgtgct 780
cagggtttga ggcacccata gacgttcggc caagggacca aggtggaat caaacgggoc 840
gccgcagaac aaaaactcat ctcagaagag gatctgaatt aa 882

```

```

<210> SEQ ID NO 390
<211> LENGTH: 279
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 390

```

```

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
 1           5           10          15
Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
 20          25          30
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
 35          40          45
Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
 50          55          60
Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
 65          70          75          80
Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
 85          90          95
Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
100          105          110
Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
115          120          125
Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
130          135          140
Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
145          150          155          160
Leu Arg Ser Lys Glu Thr Val Ala Ala Pro Ser Asp Ile Gln Met Thr
165          170          175
Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
180          185          190
Thr Cys Arg Ala Ser Gln Trp Ile Gly Ser Gln Leu Ser Trp Tyr Gln
195          200          205          210
Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Met Trp Arg Ser Ser
210          215          220
Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
225          230          235          240
Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
245          250          255
Tyr Tyr Cys Ala Gln Gly Leu Arg His Pro Lys Thr Phe Gly Gln Gly
260          265          270
Thr Lys Val Glu Ile Lys Arg
275

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<210> SEQ ID NO 391
<211> LENGTH: 837
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 391
tgcgacttgc cacagacaca tagtttggga tcaagaagaa cattgatggt attagcacia    60
atgcgtagaa tttctttggt ctcttgtcta aaggaccgtc acgacttcgg attccctcag    120
gaagagtttg gaaaccaatt ccaaaaagca gaaactattc ctgtcttgca cgaatgatc    180
cagcaaatat tcaatttgtt ttctacaaag gactcatcag ccgcttggga tgaactctg    240
ttagataaat tctacactga actatatcaa caactgaacg atctagaggc ttgcgttatt    300
caggtgtag  gagttactga aactccccta atgaaagaag attcaattct agcogttaga    360
aaatactttc agcgtatcac attgtattta aaggaaaaga aatactcccc atgtgcatgg    420
gaggtgggta gagcagaaat tatgaggtcc ttctctcttt ctacgaattt gcaagaatct    480
ttgagatcta aggaaccogt cgctgtccca tctgacatcc agatgacca gtctccatcc    540
tccctgtctg catctgtagg agaccgtgtc accatcactt gccgggcaag tcagtggatt    600
gggtctcagt tatcttggtg ccagcagaaa ccagggaaaag cccctaagct cctgatcatg    660
tggcgttcct cgttgcaaag tgggggtccca tcacgtttca gtggcagtgg atctgggaca    720
gatttcactc tcaccatcag cagtctgcaa cctgaagatt ttgctacgta ctactgtgct    780
caggttttga ggcaccta gacgttggc caagggacca aggtggaat caaacgg    837

```

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<210> SEQ ID NO 392
<211> LENGTH: 293
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 392
Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
 1             5             10             15
Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
 20             25             30
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
 35             40             45
Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
 50             55             60
Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
 65             70             75             80
Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
 85             90             95
Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
 100            105            110
Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
 115            120            125
Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
 130            135            140
Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
 145            150            155            160
Leu Arg Ser Lys Glu Thr Val Ala Ala Pro Ser Asp Ile Gln Met Thr

```





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```

tccctgtctg catctgtagg agaccgtgtc accatcactt gccgggcaag tcagtggatt    600
gggtctcagt tatcttgta ccagcagaaa ccagggaaag cccctaagct cctgatcatg    660
tggcgttcct cgttgcaaaag tggggtocca tcacgtttca gtggcagtgg atctgggaca    720
gatttcactc tcaccatcag cagtctgcaa cctgaagatt ttgctacgta ctactgtgct    780
cagggcttta tgaagcctat gacgttcggc caagggacca aggtggaat caaacgg      837

```

```

<210> SEQ ID NO 396
<211> LENGTH: 293
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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```

<400> SEQUENCE: 396

```

```

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
 1           5           10          15
Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
 20          25          30
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
 35          40          45
Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
 50          55          60
Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
 65          70          75          80
Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
 85          90          95
Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
100         105         110
Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
115         120         125
Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
130         135         140
Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
145         150         155         160
Leu Arg Ser Lys Glu Thr Val Ala Ala Pro Ser Asp Ile Gln Met Thr
165         170         175
Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
180         185         190
Ser Cys Arg Ala Ser Gln Trp Ile Gly Ser Gln Leu Ser Trp Tyr Gln
195         200         205
Gln Lys Pro Gly Glu Ala Pro Lys Leu Leu Ile Met Trp Arg Ser Ser
210         215         220
Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
225         230         235         240
Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
245         250         255
Tyr Tyr Cys Ala Gln Gly Ala Ala Leu Pro Arg Thr Phe Gly Gln Gly
260         265         270
Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Glu Gln Lys Leu Ile Ser
275         280         285
Glu Glu Asp Leu Asn
290

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<210> SEQ ID NO 397

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<211> LENGTH: 882  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 397

```

tgcgacttgc cacagacaca tagtttggga tcaagaagaa cattgatggt attagcacia    60
atgcgtagaa tttctttggt ctcttgctca aaggaccgtc acgacttcgg attccctcag    120
gaagagtttg gaaaccaatt ccaaaaagca gaaactattc ctgtcttgca cgaaatgatc    180
cagcaaatat tcaatttggt ttctacaaag gactcatcag ccgcttggga tgaactctg    240
ttagataaat tctacactga actatatcaa caactgaacg atctagagge ttgcgttatt    300
caggggtgtag gagttactga aactccocta atgaaagaag attcaattct agccgtaga    360
aaatactttc agcgtatcac attgtattta aaggaaaaga aatactcccc atgtgcatgg    420
gaggtgggta gagcagaaat tatgaggtcc ttctctcttt ctacgaattt gcaagaatct    480
ttgagatcta aggaaccogt cgctgctcca tctgacatcc agatgaccca gtctccatcc    540
tccctgtctg catctgtagg agaccgtgtc accatctctt gccgggcaag tcagtggtatt    600
gggtctcagt tatcttggtg ccagcagaaa ccagggggaag ccctaagct cctgatcatg    660
tggcgttcct cgttgcaaag tggggtocca tcacgtttca gtggcagtgg atctgggaca    720
gatttcactc tcaccatcag cagtctgcaa cctgaagatt ttgctacgta ctactgtgct    780
cagggtgctg cgttgcttag gacgttcggc caagggacca aggtggaaat caaacgggctg    840
gccgcagaac aaaaactcat ctcagaagag gatctgaatt aa                        882

```

<210> SEQ ID NO 398  
 <211> LENGTH: 279  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 398

```

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
  1           5           10           15
Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
  20           25           30
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
  35           40           45
Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
  50           55           60
Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
  65           70           75           80
Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
  85           90           95
Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
  100          105          110
Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
  115          120          125
Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
  130          135          140
Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
  145          150          155          160
Leu Arg Ser Lys Glu Thr Val Ala Ala Pro Ser Asp Ile Gln Met Thr

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165	170	175
Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile 180 185 190		
Ser Cys Arg Ala Ser Gln Trp Ile Gly Ser Gln Leu Ser Trp Tyr Gln 195 200 205		
Gln Lys Pro Gly Glu Ala Pro Lys Leu Leu Ile Met Trp Arg Ser Ser 210 215 220		
Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr 225 230 235 240		
Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr 245 250 255		
Tyr Tyr Cys Ala Gln Gly Ala Ala Leu Pro Arg Thr Phe Gly Gln Gly 260 265 270		
Thr Lys Val Glu Ile Lys Arg 275		

<210> SEQ ID NO 399  
 <211> LENGTH: 837  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 399

```

tgcgacttgc cacagacaca tagtttggga tcaagaagaa cattgatggt attagcacia    60
atgcgtagaa tttctttggt ctctgttcta aaggaccgtc acgacttcgg attccctcag    120
gaagagtttg gaaaccaatt ccaaaaagca gaaactattc ctgtcttgca cgaaatgatc    180
cagcaaatat tcaatttgtt ttctacaaag gactcatcag ccgcttggga tgaactctg    240
ttagataaat tctacactga actatatcaa caactgaacg atctagaggc ttgcgttatt    300
cagggtgtag gagttactga aactccocta atgaaagaag attcaattct agccgttaga    360
aaatactttc agcgtatcac attgtattta aaggaaaaga aatactcccc atgtgcatgg    420
gaggtgggta gagcagaat tatgagggtc ttctctcttt ctacgaattt gcaagaatct    480
ttgagatcta aggaaccgt cgctgtctca tctgacatcc agatgaccca gtctccatcc    540
tccctgtctg catctgtagg agaccgtgtc accatctctt gccgggcaag tcagtggatt    600
gggtctcagt tatcttggtt ccagcagaaa ccaggggaag cccctaagct cctgatcatg    660
tgggcttctc cgttgcaaag tggggtccca tcacgtttca gtggcagtgg atctgggaca    720
gatttcactc tcaccatcag cagtctgcaa cctgaagatt ttgctacgta ctactgtgct    780
cagggtgcgg cgttgcctag gacgttcggc caagggacca aggtggaat caaacgg      837
    
```

<210> SEQ ID NO 400  
 <211> LENGTH: 293  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 400

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met 1 5 10 15		
Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp 20 25 30		
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln 35 40 45		

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Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe  
 50 55 60  
 Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu  
 65 70 75 80  
 Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu  
 85 90 95  
 Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys  
 100 105 110  
 Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu  
 115 120 125  
 Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg  
 130 135 140  
 Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser  
 145 150 155 160  
 Leu Arg Ser Lys Glu Thr Val Ala Ala Pro Ser Asp Ile Gln Met Thr  
 165 170 175  
 Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile  
 180 185 190  
 Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Thr Leu Ser Trp Tyr Gln  
 195 200 205  
 Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Trp Phe Gly Ser Arg  
 210 215 220  
 Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr  
 225 230 235 240  
 Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr  
 245 250 255  
 Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly  
 260 265 270  
 Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Glu Gln Lys Leu Ile Ser  
 275 280 285  
 Glu Glu Asp Leu Asn  
 290

&lt;210&gt; SEQ ID NO 401

&lt;211&gt; LENGTH: 882

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 401

tgcgacttgc cacagacaca tagtttggga tcaagaagaa cattgatggt attagcacia 60  
 atgcgtagaa tttctttggt ctcttgtcta aaggaccgct acgacttcgg attccctcag 120  
 gaagagtttg gaaaccaatt ccaaaaagca gaaactattc ctgtcttgca cgaaatgatc 180  
 cagcaaatat tcaatttgggt ttctacaaag gactcatcag ccgcttggga tgaactctg 240  
 ttagataaat tctacactga actatatcaa caactgaacg atctagagggc ttgcgttatt 300  
 cagggtgtag gagttactga aactccccta atgaaagaag attcaattct agccgttaga 360  
 aaatactttc agcgtatcac attgtattta aaggaaaaga aatactcccc atgtgcatgg 420  
 gaggtgggta gagcagaaat tatgaggtcc ttctctcttt ctacgaattt gcaagaatct 480  
 ttgagatcta aggaaaccgt cgctgtccca tctgacatcc agatgaccca gtctccatcc 540  
 tccctgtctg catctgtagg agaccgtgtc accatcaact gccgggcaag tcgtccgatt 600

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gggacgacgt taagttggtgta ccagcagaaa ccagggaaaag cccctaagct cctgatctgg 660
tttggttccc ggttgcaaaag tggggtoccca tcacgtttca gtggcagtgg atctgggaca 720
gatttcactc tcaccatcag cagtctgcaa cctgaagatt ttgctacgta ctactgtgcg 780
caggctggga cgcacacctac gacgttcggc caagggacca aggtggaat caaacgggcg 840
gccgcagaac aaaaactcat ctcagaagag gatctgaatt aa 882

```

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<210> SEQ ID NO 402
<211> LENGTH: 279
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

```

```

<400> SEQUENCE: 402

```

```

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
 1           5           10           15
Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
 20           25           30
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
 35           40           45
Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
 50           55           60
Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
 65           70           75           80
Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
 85           90           95
Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
100           105           110
Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
115           120           125
Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
130           135           140
Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
145           150           155           160
Leu Arg Ser Lys Glu Thr Val Ala Ala Pro Ser Asp Ile Gln Met Thr
165           170           175
Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
180           185           190
Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Thr Leu Ser Trp Tyr Gln
195           200           205
Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Trp Phe Gly Ser Arg
210           215           220
Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr
225           230           235           240
Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr
245           250           255
Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly
260           265           270
Thr Lys Val Glu Ile Lys Arg
275

```

```

<210> SEQ ID NO 403
<211> LENGTH: 837
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence

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&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 403

```

tgcgacttgc cacagacaca tagtttggga tcaagaagaa cattgatggt attagcacia    60
atgcgtagaa tttctttggt ctcttctcta aaggaccgtc acgacttcgg attccctcag    120
gaagagtttg gaaaccaatt ccaaaaagca gaaactattc ctgtcttgca cgaaatgatc    180
cagcaaatat tcaatttgggt ttctacaaag gactcatcag ccgcttggga tgaactctg    240
ttagataaat tctacactga actatatcaa caactgaacg atctagaggg ttgcgttatt    300
caggggtgtag gagttactga aactccocta atgaaagaag attcaattct agccgttaga    360
aaatactttc agcgtatcac attgtattta aaggaaaaga aatactcccc atgtgcatgg    420
gaggtgggta gagcagaaat tatgaggtcc ttctctcttt ctacgaattt gcaagaatct    480
ttgagatcta aggaaaccgt cgctgctcca tctgacatcc agatgaccca gtctccatcc    540
tccctgtctg catctgtagg agaccgtgtc accatcactt gccgggcaag tcgtccgatt    600
gggacgacgt taagtgggta ccagcagaaa ccagggaaag ccctaagct cctgatctgg    660
tttggttccc ggttgcaaag tggggtocca tcacgtttca gtggcagtgg atctgggaca    720
gatttcactc tcaccatcag cagtctgcaa cctgaagatt ttgctacgta ctactgtgcg    780
caggtgggga cgcatectac gacgttcggc caagggacca aggtggaat caaacgg      837

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&lt;210&gt; SEQ ID NO 404

&lt;211&gt; LENGTH: 293

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 404

```

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
 1          5          10          15
Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
          20          25          30
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
          35          40          45
Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
          50          55          60
Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
          65          70          75          80
Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
          85          90          95
Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
          100          105          110
Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
          115          120          125
Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
          130          135          140
Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
          145          150          155          160
Leu Arg Ser Lys Glu Thr Val Ala Ala Pro Ser Asp Ile Gln Met Thr
          165          170          175
Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
          180          185          190

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Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met Leu Ser Trp Tyr Gln  
 195 200 205  
 Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Leu Phe Gly Ser Arg  
 210 215 220  
 Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr  
 225 230 235 240  
 Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr  
 245 250 255  
 Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly  
 260 265 270  
 Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Glu Gln Lys Leu Ile Ser  
 275 280 285  
 Glu Glu Asp Leu Asn  
 290

<210> SEQ ID NO 405  
 <211> LENGTH: 882  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 405

tgcgacttgc cacagacaca tagtttggga tcaagaagaa cattgatggt attagcacia 60  
 atgcgtagaa tttctttggt ctctgtcta aaggaccgtc acgacttcgg attccctcag 120  
 gaagagtttg gaaaccaatt ccaaaaagca gaaactattc ctgtcttgca cgaatgatc 180  
 cagcaaatat tcaatttgtt ttctacaaag gactcatcag ccgcttggga tgaactctg 240  
 ttagataaat tctacactga actatatcaa caactgaacg atctagaggc ttgogttatt 300  
 cagggtgtag gagttactga aactccccta atgaaagaag attcaattct agccgtaga 360  
 aaatacttcc agcgtatcac attgtattta aaggaaaaga aatactcccc atgtgcatgg 420  
 gaggtgggta gagcagaaat tatgaggtcc ttctctcttt ctacgaattt gcaagaatct 480  
 ttgagatcta aggaaaccgt cgctgtccca tctgacatcc agatgaccca gtctccatcc 540  
 tccctgtctg catctgtagg agaccgtgtc accatcactt gccgggcaag tegtccgatt 600  
 gggacgatgt taagtgggta ccagcagaaa ccagggaaag cccctaagct cctgatcttg 660  
 tttggttccc ggttgcaaag tggggtocca tcacgtttca gtggcagtgg atctgggaca 720  
 gatttcactc tcaccatcag cagtctgcaa cctgaagatt ttgctacgta ctactgtgcg 780  
 caggctggga cgcacacctac gacgttggc caagggacca aggtggaat caaacgggcg 840  
 gccgcagaac aaaaactcat ctcaagaag gatctgaatt aa 882

<210> SEQ ID NO 406  
 <211> LENGTH: 279  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 406

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met  
 1 5 10 15  
 Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp  
 20 25 30  
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln  
 35 40 45

-continued

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe  
 50 55 60  
 Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu  
 65 70 75 80  
 Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu  
 85 90 95  
 Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys  
 100 105 110  
 Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu  
 115 120 125  
 Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg  
 130 135 140  
 Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser  
 145 150 155 160  
 Leu Arg Ser Lys Glu Thr Val Ala Ala Pro Ser Asp Ile Gln Met Thr  
 165 170 175  
 Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile  
 180 185 190  
 Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met Leu Ser Trp Tyr Gln  
 195 200 205  
 Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Leu Phe Gly Ser Arg  
 210 215 220  
 Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr  
 225 230 235 240  
 Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr  
 245 250 255  
 Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly  
 260 265 270  
 Thr Lys Val Glu Ile Lys Arg  
 275

&lt;210&gt; SEQ ID NO 407

&lt;211&gt; LENGTH: 837

&lt;212&gt; TYPE: DNA

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 407

tgcgacttgc cacagacaca tagtttggga tcaagaagaa cattgatggt attagcaca 60  
 atgcgtagaa tttctttggt ctcttgctca aaggaccgtc acgacttcgg attccctcag 120  
 gaagagtttg gaaaccaatt ccaaaaagca gaaactattc ctgtcttgca cgaaatgatc 180  
 cagcaaatat tcaatttgggt ttctacaaag gactcatcag ccgcttggga tgaaactctg 240  
 ttagataaat tctacactga actatatcaa caactgaacg atctagaggc ttgcgttatt 300  
 cagggtgtag gagttactga aactccocta atgaaagaag attcaattct agccgttaga 360  
 aaatactttc agcgtatcac attgtattta aaggaaaaga aatactcccc atgtgcatgg 420  
 gaggtgggta gagcagaat tatgaggtcc ttctctcttt ctacgaattt gcaagaatct 480  
 ttgagatcta aggaaaccgt cgctgtcca tctgacatcc agatgaccca gtctccatcc 540  
 tccctgtctg catctgtagg agaccgtgtc accatcaact gccgggcaag tcgtccgatt 600  
 gggacgatgt taagttggta ccagcagaaa ccagggaaag cccctaagct cctgatcttg 660  
 tttggttccc ggttgcaaag tggggtccca tcacgtttca gtggcagtgg atctgggaca 720

-continued

gatttcactc tcaccatcag cagtctgcaa cctgaagatt ttgctacgta ctactgtgcg 780

caggctggga cgcacccctac gacgttcggc caagggacca aggtggaat caaacgg 837

<210> SEQ ID NO 408

<211> LENGTH: 293

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 408

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met  
1 5 10 15

Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp  
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln  
35 40 45

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe  
50 55 60

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu  
65 70 75 80

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu  
85 90 95

Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys  
100 105 110

Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu  
115 120 125

Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg  
130 135 140

Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser  
145 150 155 160

Leu Arg Ser Lys Glu Thr Val Ala Ala Pro Ser Asp Ile Gln Met Thr  
165 170 175

Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile  
180 185 190

Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met Leu Ser Trp Tyr Gln  
195 200 205

Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Leu Ala Phe Ser Arg  
210 215 220

Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr  
225 230 235 240

Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr  
245 250 255

Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly  
260 265 270

Thr Lys Val Glu Ile Lys Arg Ala Ala Ala Glu Gln Lys Leu Ile Ser  
275 280 285

Glu Glu Asp Leu Asn  
290

<210> SEQ ID NO 409

<211> LENGTH: 882

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Derived from a Human Germline sequence.

-continued

&lt;400&gt; SEQUENCE: 409

```

tgcgacttgc cacagacaca tagtttggga tcaagaagaa cattgatggt attagcacia    60
atgcgtagaa tttctttggt ctcttgtcta aaggaccgtc acgacttcgg attccctcag    120
gaagagtttg gaaaccaatt ccaaaaagca gaaactattc ctgtcttgca cgaatgatc    180
cagcaaatat tcaatttgggt ttctacaaag gactcatcag cgccttggga tgaaactctg    240
ttagataaat tctacactga actatatcaa caactgaacg atctagagggc ttgcgttatt    300
caggggtgag gagttactga aactccocta atgaaagaag attcaattct agccgttaga    360
aaatactttc agcgtatcac attgtattta aaggaaaaga aatactcccc atgtgcatgg    420
gaggtgggta gagcagaat tatgaggtcc ttctctcttt ctacgaattt gcaagaatct    480
ttgagateta aggaaccogt cgtgtctcca tctgacatcc agatgaccca gtctccatcc    540
tcctctgtct catctgtagg agaccgtgtc accatcactt gccgggcaag tcgtccgatt    600
gggacgatgt taagttggtg ccagcagaaa ccagggaag cccctaagct cctgatcctt    660
gctttttccc gtttgcaaag tggggtocca tcacgtttca gtggcagtgg atctgggaca    720
gatttcactc tcaccatcag cagtctgcaa cctgaagatt ttgctacgta ctactgcgcg    780
caggtcggga cgcacatcac gacgttcggc caagggacca aggtggaat caaacgggcg    840
gccgcagaac aaaaactcat ctcaagaag gatctgaatt aa                        882

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&lt;210&gt; SEQ ID NO 410

&lt;211&gt; LENGTH: 279

&lt;212&gt; TYPE: PRT

&lt;213&gt; ORGANISM: Artificial Sequence

&lt;220&gt; FEATURE:

&lt;223&gt; OTHER INFORMATION: Derived from a Human Germline sequence.

&lt;400&gt; SEQUENCE: 410

```

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Ser Arg Arg Thr Leu Met
 1          5          10          15
Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp
          20          25          30
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
          35          40          45
Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
          50          55          60
Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
          65          70          75          80
Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
          85          90          95
Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met Lys
          100          105          110
Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr Leu
          115          120          125
Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
          130          135          140
Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu Ser
          145          150          155          160
Leu Arg Ser Lys Glu Thr Val Ala Ala Pro Ser Asp Ile Gln Met Thr
          165          170          175
Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile
          180          185          190

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Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met Leu Ser Trp Tyr Gln  
           195                                  200                                  205  
 Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile Leu Ala Phe Ser Arg  
           210                                  215                                  220  
 Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr  
           225                                  230                                  235                                  240  
 Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr  
                                   245                                  250                                  255  
 Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr Thr Phe Gly Gln Gly  
                                   260                                  265                                  270  
 Thr Lys Val Glu Ile Lys Arg  
           275

<210> SEQ ID NO 411  
 <211> LENGTH: 837  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 411

tgcgacttgc cacagacaca tagtttggga tcaagaagaa cattgatggt attagcacia 60  
 atgcgtagaa tttctttggt ctcttgtcta aaggaccgtc acgacttcgg attccctcag 120  
 gaagagtttg gaaaccaatt ccaaaaagca gaaactattc ctgtcttgca cgaatgatc 180  
 cagcaaatat tcaatttgtt ttctacaaag gactcatcag ccgcttggga tgaactctg 240  
 ttagataaat tctacactga actatatcaa caactgaacg atctagaggc ttgogttatt 300  
 cagggtgtag gagttactga aactccccta atgaaagaag attcaattct agccgttaga 360  
 aaatactttc agcgtatcac attgtattta aaggaaaaga aatactcccc atgtgcatgg 420  
 gaggtgggta gagcagaaat tatgaggtcc ttctctcttt ctacgaattt gcaagaatct 480  
 ttgagatceta aggaaaccgt cgctgtccca tctgacatcc agatgaccca gtctccatcc 540  
 tccctgtctg catctgtagg agaccgtgtc accatcactt gccgggcaag tcgtccgatt 600  
 gggacgatgt taagttggta ccagcagaaa ccagggaaag cccctaagct cctgatcctt 660  
 gctttttccc gtttgcaaaag tggggtocca tcacgtttca gtggcagtgg atctgggaca 720  
 gatttcactc tcaccatcag cagtctgcaa cctgaagatt ttgctacgta ctactgcgcg 780  
 caggctggga cgcacacctac gacgttggc caagggacca aggtggaat caaacgg 837

<210> SEQ ID NO 412  
 <211> LENGTH: 108  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 412

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly  
           1                                  5                                  10                                  15  
 Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Trp Ile Gly Ser Gln  
           20                                  25                                  30  
 Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile  
           35                                  40                                  45  
 Met Trp Arg Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly  
           50                                  55                                  60  
 Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro

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65	70	75	80
Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Gly Leu Arg His Pro Lys			
	85	90	95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Cys			
	100	105	

<210> SEQ ID NO 413  
 <211> LENGTH: 324  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 413

gacatccaga tgaccagtc tccatcctcc ctgtctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtca gtggattggg tctcagttat cttggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatcatgtgg cgttcctcgt tgcaaaagtg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240
gaagattttg ctacgtacta ctgtgctcag ggtttgaggc atcctaagac gttcggccaa	300
gggaccaagg tggaaatcaa atgc	324

<210> SEQ ID NO 414  
 <211> LENGTH: 108  
 <212> TYPE: PRT  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 414

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Pro Ala Ser Val Gly														
1				5					10					15
Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Arg Pro Ile Gly Thr Met														
			20					25					30	
Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile														
			35				40						45	
Leu Ala Phe Ser Arg Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly														
			50				55						60	
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro														
65				70					75					80
Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Ala Gly Thr His Pro Thr														
			85					90						95
Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg														
			100					105						

<210> SEQ ID NO 415  
 <211> LENGTH: 324  
 <212> TYPE: DNA  
 <213> ORGANISM: Artificial Sequence  
 <220> FEATURE:  
 <223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 415

gacatccaga tgaccagtc tccatcctcc ctgcctgcat ctgtaggaga ccgtgtcacc	60
atcacttgcc gggcaagtgc tccgattggg acgatgtaa gttggtacca gcagaaacca	120
gggaaagccc ctaagctcct gatccttgct ttttcccggt tgcaaaagtg ggtcccatca	180
cgtttcagtg gcagtggatc tgggacagat ttcactctca ccatcagcag tctgcaacct	240

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gaagattttg ctacgtacta ctgcgcgcag gctgggacgc atcctacgac gttcggccaa 300
gggaccaagg tggaaatcaa acgg 324

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<210> SEQ ID NO 416
<211> LENGTH: 62
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 416
gcaacagcgt cgacggacat ccagatgacc cagtctccat cctccctgcc tgcattctgta 60
gg 62

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<210> SEQ ID NO 417
<211> LENGTH: 360
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 417
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttagt cagtatagga tgcattgggt ccgccaggct 120
ccagggaaga gtctagagtg ggtctcaagt attgatacta ggggttcgct tacatactac 180
gcagaccctg tgaagggcgc gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaagctgtg 300
acgatgtttt ctcctttttt tgactactgg ggtcagggaa ccctggtcac cgtctcgagc 360

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<210> SEQ ID NO 418
<211> LENGTH: 369
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 418
gaggtgcagc tgttggagtc tgggggaggc ttggtacagc ctggggggtc cctgcgtctc 60
tcctgtgcag cctccggatt cacctttgct gattatggga tgcgttgggt ccgccaggct 120
ccagggaagg gtctagagtg ggtctcatct attacgcgga ctggctgtgt tacatactac 180
gcgactccg tgaagggcgc gttcaccatc tcccgcgaca attccaagaa cacgctgtat 240
ctgcaaatga acagcctgcg tgccgaggac accgcggtat attactgtgc gaaatggcgg 300
aatcggcatg gtgagtatct tgctgatttt gactactggg gtcagggaac cctggtcacc 360
gtctcgagc 369

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<210> SEQ ID NO 419
<211> LENGTH: 7
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

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<400> SEQUENCE: 419
Thr Val Ala Ala Pro Ser Cys
1 5

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<210> SEQ ID NO 420

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<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Synthetic Linker Sequence

<400> SEQUENCE: 420

Gly Gly Gly Gly Ser Cys
 1             5

<210> SEQ ID NO 421
<211> LENGTH: 6
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 421

Thr Val Ala Ala Pro Ser
 1             5

<210> SEQ ID NO 422
<211> LENGTH: 108
<212> TYPE: PRT
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Derived from a Human Germline sequence.

<400> SEQUENCE: 422

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val Gly
 1             5             10             15

Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Gln Trp Ile Gly Ser Gln
                20             25             30

Leu Ser Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys Leu Leu Ile
    35             40             45

Met Trp Arg Ser Ser Leu Gln Ser Gly Val Pro Ser Arg Phe Ser Gly
    50             55             60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro
 65             70             75             80

Glu Asp Phe Ala Thr Tyr Tyr Cys Ala Gln Gly Ala Ala Leu Pro Arg
                85             90             95

Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys Arg
    100             105

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The invention claimed is:

1. An anti-serum albumin immunoglobulin single variable domain comprising an amino acid sequence selected from the group consisting of: SEQ ID NO: 412 (DOM7h-14-10 R108C).

2. A multispecific ligand comprising an anti-serum albumin immunoglobulin single variable domain of claim 1, and a binding moiety that specifically binds a target antigen other than serum albumin.

3. The anti-serum albumin immunoglobulin single variable domain of claim 1, wherein the variable domain is conjugated to an NCE drug.

4. A fusion protein comprising a polypeptide or peptide drug fused to an anti-serum albumin immunoglobulin single variable domain according to claim 1.

5. The fusion protein according to claim 4, wherein the fusion protein comprises a linker between the anti-serum albumin immunoglobulin single variable domain and the polypeptide or peptide drug.

6. The fusion protein according to claim 5, wherein the linker comprises the amino acid sequence TVA between the anti-serum albumin immunoglobulin single variable domain and the polypeptide or peptide drug.

7. The fusion protein according to claim 5, wherein the linker comprises the amino acid sequence TVAAPS (SEQ ID NO: 421) between the anti-serum albumin immunoglobulin single variable domain and the polypeptide or peptide drug.

8. A composition comprising the anti-serum albumin immunoglobulin single variable domain of claim 1, and a pharmaceutically acceptable diluent, carrier, excipient or vehicle.

9. A composition comprising the anti-serum albumin immunoglobulin single variable domain of claim 2, and a pharmaceutically acceptable diluent, carrier, excipient or vehicle.

10. A composition comprising the anti-serum albumin immunoglobulin single variable domain of claim 3, and a pharmaceutically acceptable diluent, carrier, excipient or vehicle.

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11. A composition comprising the anti-serum albumin immunoglobulin single variable domain of claim 4, and a pharmaceutically acceptable diluent, carrier, excipient or vehicle.

12. A composition comprising the anti-serum albumin immunoglobulin single variable domain of claim 5, and a pharmaceutically acceptable diluent, carrier, excipient or vehicle.

13. A composition comprising the anti-serum albumin immunoglobulin single variable domain of claim 6, and a pharmaceutically acceptable diluent, carrier, excipient or vehicle.

14. A composition comprising the anti-serum albumin immunoglobulin single variable domain of claim 7, and a pharmaceutically acceptable diluent, carrier, excipient or vehicle.

15. An anti-serum albumin immunoglobulin single variable domain comprising comprising an amino acid sequence selected from the group consisting of: SEQ ID NO: 2 (DOM7h-14-18), SEQ ID NO: 3 (DOM7h-14-19), SEQ ID NO: 4 (DOM7h-14-28), and SEQ ID NO: 5 (DOM7h-14-36).

16. A multispecific ligand comprising an anti-serum albumin immunoglobulin single variable domain of claim 15, and a binding moiety that specifically binds a target antigen other than serum albumin.

17. The anti-serum albumin immunoglobulin single variable domain of claim 16, wherein the variable domain is conjugated to an NCE drug.

18. A fusion protein comprising a polypeptide or peptide drug fused to an anti-serum albumin immunoglobulin single variable domain according to claim 16.

19. The fusion protein according to claim 18, wherein the fusion protein comprises a linker between the anti-serum albumin immunoglobulin single variable domain and the polypeptide or peptide drug.

20. The fusion protein according to claim 19, wherein the linker comprises the amino acid sequence TVA between the

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anti-serum albumin immunoglobulin single variable domain and the polypeptide or peptide drug.

21. The fusion protein according to claim 19, wherein the linker comprises the amino acid sequence TVAAPS (SEQ ID NO: 421) between the anti-serum albumin immunoglobulin single variable domain and the polypeptide or peptide drug.

22. A composition comprising the anti-serum albumin immunoglobulin single variable domain of claim 15, and a pharmaceutically acceptable diluent, carrier, excipient or vehicle.

23. A composition comprising the anti-serum albumin immunoglobulin single variable domain of claim 16, and a pharmaceutically acceptable diluent, carrier, excipient or vehicle.

24. A composition comprising the anti-serum albumin immunoglobulin single variable domain of claim 17, and a pharmaceutically acceptable diluent, carrier, excipient or vehicle.

25. A composition comprising the anti-serum albumin immunoglobulin single variable domain of claim 18, and a pharmaceutically acceptable diluent, carrier, excipient or vehicle.

26. A composition comprising the anti-serum albumin immunoglobulin single variable domain of claim 19, and a pharmaceutically acceptable diluent, carrier, excipient or vehicle.

27. A composition comprising the anti-serum albumin immunoglobulin single variable domain of claim 20, and a pharmaceutically acceptable diluent, carrier, excipient or vehicle.

28. A composition comprising the anti-serum albumin immunoglobulin single variable domain of claim 21, and a pharmaceutically acceptable diluent, carrier, excipient or vehicle.

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